

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 23, 2004, 02:14:00 ; Search time 7417.52 Seconds
(without alignments)
12559.330 Million cell updates/sec

Title: US-09-830-972-28
Perfect score: 3833
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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8: em_htc:*
9: gb_est1:*
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22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*

28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	% Query Match	Length	DB	ID	Description
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1	986	25.7	1798	11	AF125103	AF125103 Homo sapi
2	915.6	23.9	1785	11	AF077050	AF077050 Homo sapi
3	774.2	20.2	3533	11	AK034902	AK034902 Mus muscu
c 4	668.6	17.4	956	9	AL573494	AL573494 AL573494
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6	631	16.5	871	13	BQ719894	BQ719894 AGENCOURT
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36	552	14.4	785	14	CA511870	CA511870 UI-R-FJ0-
37	552	14.4	817	14	CA322433	CA322433 UI-M-FX0-
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ALIGNMENTS

RESULT 1

AF125103

LOCUS AF125103 1798 bp mRNA linear HTC 22-MAY-2001

DEFINITION Homo sapiens neuroendocrine specific protein c homolog mRNA,
complete cds.

ACCESSION AF125103

VERSION AF125103.1 GI:5107001

KEYWORDS HTC.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1798)

AUTHORS Zhang,Q.H., Ye,M., Wu,X.Y., Ren,S.X., Zhao,M., Zhao,C.J., Fu,G.,
Shen,Y., Fan,H.Y., Lu,G., Zhong,M., Xu,X.R., Han,Z.G., Zhang,J.W.,
Tao,J., Huang,Q.H., Zhou,J., Hu,G.X., Gu,J., Chen,S.J. and Chen,Z.
TITLE Cloning and functional analysis of cDNAs with open reading frames
for 300 previously undefined genes expressed in CD34+ hematopoietic
stem/progenitor cells

JOURNAL Genome Res. 10 (10), 1546-1560 (2000)

MEDLINE 20499367

PUBMED 11042152

REFERENCE 2 (bases 1 to 1798)

AUTHORS Ye,M., Zhang,Q., Zhou,J., Shen,Y., Guan,Z., Wu,X., Fan,H., Mao,H.,
Dai,M., Huang,Q., Chen,S. and Chen,Z.

TITLE Human neuroendocrine specific protein c homolog mRNA, complete cds

JOURNAL Unpublished

REFERENCE 3 (bases 1 to 1798)

AUTHORS Ye,M., Zhang,Q., Zhou,J., Shen,Y., Guan,Z., Wu,X., Fan,H., Mao,H.,
Dai,M., Huang,Q., Chen,S. and Chen,Z.

TITLE Direct Submission

JOURNAL Submitted (02-FEB-1999) Shanghai Institute of Hematology, Shanghai
Second Medical University, Rui-Jin Hospital, 197 Rui-Jin Road II,
Shanghai 200025, P. R. China

FEATURES Location/Qualifiers

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ORIGIN

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AF077050
 LOCUS AF077050 1785 bp mRNA linear HTC 21-NOV-2002
 DEFINITION Homo sapiens neuroendocrine-specific protein C homolog mRNA, complete cds.
 ACCESSION AF077050
 VERSION AF077050.1 GI:4689147
 KEYWORDS HTC..
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1785)
 AUTHORS Song,H., Peng,Y., Zhou,J., Huang,Q., Dai,M., Mao,Y., Yu,Y., Xu,X., Luo,B., Hu,R. and Chen,J.
 TITLE Human neuroendocrine-specific protein C (NSP) homolog gene
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1785)
 AUTHORS Song,H.
 TITLE Direct Submission
 JOURNAL Submitted (10-JUL-1998) Rui-Jin Hospital, Shanghai Institute of Endocrinology, Molecular Medical Center, 197 Rui-Jin Road II, Shanghai 200025, P.R. China
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 BASE COUNT 520 a 316 c 402 g 547 t
 ORIGIN

Query Match 23.9%; Score 915.6; DB 11; Length 1785;
 Best Local Similarity 85.5%; Pred. No. 4.6e-121;
 Matches 1238; Conservative 0; Mismatches 144; Indels 66; Gaps 17;

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Qy      2304 GTTGGTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGC 2363
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Qy      2364 TTGTTCTGCTGCTCTCGCTGACAGTATTTCAGCATTGTGAGTGTAACGGCCTACATTGCC 2423
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Qy      2424 TTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAGGCTATC 2483
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Qy	2664		ATGTGGGTATTTACCTATGTTGGTGCCTTGTTCATGGTCTGACACTACTAATTTTGGCT	2723
Db	607		ATGTGGGTATTTACCTATGTTGGTGCCTTGTTCATGGTCTGACACTACTGATTTTGGCT	666
Qy	2724		CTGATTTCACTCTTCAGTGTTCTGTTATTTATGAACGGCATCAGGCGCAAATAGATCAT	2783
Db	667		CTCATTTCACTCTTCAGTGTTCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT	726
Qy	2784		TATCTGGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATC	2843
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JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
 MEDLINE 20499374
 PUBMED 11042159
 REFERENCE 3
 AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
 Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
 Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
 Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
 Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
 Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
 Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
 TITLE RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer
 JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
 MEDLINE 20530913
 PUBMED 11076861
 REFERENCE 4
 AUTHORS Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,
 Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
 Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I.,
 Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R.,
 Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T.,
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 Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G.,
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 Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C.,
 Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D.,
 Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P.,
 Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P.,
 Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H.,
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 Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L.,
 Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
 and Hayashizaki,Y.
 TITLE Functional annotation of a full-length mouse cDNA collection
 JOURNAL Nature 409 (6821), 685-690 (2001)
 MEDLINE 21085660
 PUBMED 11217851
 REFERENCE 5
 AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research
 Group Phase I & II Team.
 TITLE Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 JOURNAL Nature 420, 563-573 (2002)
 REFERENCE 6 (bases 1 to 3533)
 AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
 Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
 Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
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 Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
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 Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
 Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,

Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.

FEATURES Location/Qualifiers

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/note="RETICULON 4 (NEURITE OUTGROWTH INHIBITOR) (NOGO
PROTEIN) (FOOCEN) (GLUT4 VESICLE 20 KDA PROTEIN) homolog
[Rattus norvegicus] (SWISSPROT|Q9JK11, evidence: FASTY,
95.8%ID, 100%length, match=1068)"

BASE COUNT 955 a 774 c 840 g 964 t

ORIGIN

Query Match 20.2%; Score 774.2; DB 11; Length 3533;
Best Local Similarity 78.3%; Pred. No. 5.1e-101;
Matches 1190; Conservative 0; Mismatches 258; Indels 71; Gaps 19;

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Qy 2424 TTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAGGCTATC 2483
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Db 860 TTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAGGCTATC 919
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Qy 2484 CAGAAATCTGATGAAGGCCACCCATTTCAGGGCATATTTGGAATCTGAAGTTGCTATATCT 2543
|||||

Db 920 CAGAAATCAGATGAAGGCCACCCATTTCAGGGCATATTTGGAATCTGAAGTTGCCATATCA 979
|||||

Qy	2544	GAGGAGTTTGGTTTCAGAAAGTACAGCAATTCTGCTCTTGGTCATGTTAACTGCACAATAAAAA	2603
Db	980	GAGGAATTGGTTTCAGAAATATAGTAATTCTGCTCTTGGTCATGTGAACAGCACAATAAAAA	1039
Qy	2604	GAACTCAGACGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTG	2663
Db	1040	GAATTGAGGCGTCTCTTCTTAGTTGATGATTTAGTTGATTCCCTGAAGTTTGCAGTGTTG	1099
Qy	2664	ATGTGGGTATTTACCTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTAATTTTGGCT	2723
Db	1100	ATGTGAGTATTTACTTACGTTGGTGCCTTGTTCAATGGTTTGACACTACTGATTTTAGCT	1159
Qy	2724	CTGATTTCACTCTTCAGTGTTCCGTGTTATTTATGAACGGCATCAGGCGCAAATAGATCAT	2783
Db	1160	CTGATCTCACTCTTCAGTATTCCGTGTTATATATGAACGGCATCAGGCGCAGATAGATCAT	1219
Qy	2784	TATCTGGGACTTGC AAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATC	2843
Db	1220	TATCTAGGACTTGC AAAACAAGAGCGTTAAGGATGCCATGGCCAAAATCCAAGCAAAAATC	1279
Qy	2844	CCTGGATTGAAGCGTAAAGCTGAATGAGAAAGCCTGAAAGAGTTAACAATAGAGGAGTTT	2903
Db	1280	CCTGGATTGAAGCGCAAAGCAGAATGAAAAGGCCCAAACAGTAGACA-----TTC	1330
Qy	2904	ATCTTTAAAGGGGATATTCATTTGATTCCATTG-GGGAGGGTCAGGGAAGAACAAAGCCT	2962
Db	1331	ATCTTTAAAGGGGACACTCCCTTGGTTACGGGGTGGGCGGGTCAGGGGTGAGCCCTGGGT	1390
Qy	2963	TGACATTGCAGTGCAGTTTTCACAGATCTTTATTTTTAGCAACGCAGTGTCTGAGGAAAAA	3022
Db	1391	GGCCGTGCAGTTTCAG-----TTATTTTTAGCAGTGCAGTGTCTGAGGAAAAA	1438
Qy	3023	TGACCTGTCTTGACTGCCCTGTGTTTCATCATCTTAAGTATTGTAAGCTGCTATGTATGGA	3082
Db	1439	TTACCTGTCTTGACT-TCCTGTGTTTATCATCTTAAGTATTGTAAGCTGCTGTGTATGGA	1497
Qy	3083	TTTAAATCGTAATCATATTTGTTTTTCCCTGTATGAGGCACTGGTGAATAAACAAAGATCT	3142
Db	1498	TCT-CATGTAGTCATACTTGTTTTCCCCAGATGAGGCACTTGGTGAATAAAAGGATG-CT	1555
Qy	3143	GAGAAAGCTGTATATTACACTTTGTGCGAGGTAGTCTTGCTGTATTTGGGGAATTGCAAA	3202
Db	1556	GGGAAAACGTGTGTGTTATATTCTGTTGCAGGTAGTCTGGCTGTATTTGGAAAGTTGCAAA	1615
Qy	3203	GAAAGTGGA----GCTGACAGAAATAACCCCTTTTCACAGTTTGTGCACTGTGTACGGTCT	3258
Db	1616	GAAGGTAGATTTGGGGGCAGGAAAAACAACCCCTTTTCACAGTGTACTGTGTTTGGTTGGT	1675
Qy	3259	GTGTAGGTGTGATGCAGATTTTCTGAAATGAAATGTTTAGACGAGATCATGCCCAAGGC	3318
Db	1676	GTAAACTGATGCAGATTTTCTGAAATGAGATGTTTAGATGAG--CATACTACTAAAGC	1733
Qy	3319	AGGAGTGAAAAAGCTTGCCTTTCCCTGGTATGTTCTAGGTGTATTGTGAAATTTACTGTTG	3378
Db	1734	AGAGTGGA AAAATCTGTGCT--TTTATGGTATGTTCTAGGTGTATTGTGATTTACTGTG----	1788

http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0DI051CA06NP1&cluster=1423.r. Contact :
 Feng Liang Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CS0DI051CA06NP1.

```

FEATURES
  source          Location/Qualifiers
                  1. .956
                  /organism="Homo sapiens"
                  /mol_type="mRNA"
                  /db_xref="taxon:9606"
                  /clone="CS0DI051YB11"
                  /tissue_type="PLACENTA COT 25-NORMALIZED"
                  /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                  /note="1st strand cDNA was primed with a NotI-oligo(dT)
                  primer. Five prime end enriched, double-strand cDNA was
                  digested with Not I and cloned into the Not I and EcoR V
                  sites of the pCMVSPORT 6 vector. Library was normalized."

BASE COUNT      283 a      219 c      207 g      237 t      10 others
ORIGIN

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Query Match 17.4%; Score 668.6; DB 9; Length 956;
 Best Local Similarity 88.7%; Pred. No. 8.5e-86;
 Matches 795; Conservative 3; Mismatches 67; Indels 31; Gaps 6;

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Qy      2304 GTTGTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGC 2363
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Db      878 GTTGTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGC 819

Qy      2364 TTGTTCTGCTGCTCTCGCTGACAGTATTTCAGCATTGTGAGTGTAACGGCCTACATTGCC 2423
          | |||
Db      818 CTATTCCTGCTGCTTTTCATTRACAGTATTTCAGCATTGTGAGCGTAACAGCCTACATTGCC 759

Qy      2424 TTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAGGCTATC 2483
          |||
Db      758 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC 699

Qy      2484 CAGAAATCTGATGAAGGCCACCCATTTCAGGGCATATTTGGAATCTGAAGTTGCTATATCT 2543
          |||
Db      698 CAGAAATCAGATGAAGGCCACCCATTTCAGGGCATATCTGGAATCTGAAGTTGCTATATCT 639

Qy      2544 GAGGAGTTGGTTCAGAAGTACAGCAATTCTGCTCTTGGTCATGTGTAAGTGCACAATAAAA 2603
          |||
Db      638 GAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAACTGCACGATAAAG 579

Qy      2604 GAACTCAGACGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTG 2663
          |||
Db      578 GAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTG 519

Qy      2664 ATGTGGGTATTTACCTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTAATTTTGGCT 2723
          |||
Db      518 ATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAAATGGTCTGACACTACTGATTTTGGCT 459

Qy      2724 CTGATTTCACTCTTCAGTGTTCTGTTATTTATGAACGGCATCAGGCGCAAATAGATCAT 2783
          ||
Db      458 CTCATTTCACTCTTCAGTGTTCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT 399

Qy      2784 TATCTGGGACTTGCAAATAAGAAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATC 2843

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FEATURES                      Location/Qualifiers
    source                    1. .646
                              /organism="Bos taurus"
                              /mol_type="mRNA"
                              /db_xref="taxon:9913"
                              /tissue_type="pooled"
                              /lab_host="DH10B"
                              /clone_lib="MARC 6BOV"
                              /note="Vector: pCDNA3.1; Site_1: EcoRI; Site_2: NotI;
Library made with RNA pooled from multiple tissues
including liver, lung, hypothalamus, pituitary, and
placenta/endometrium."
BASE COUNT      207 a      114 c      122 g      203 t
ORIGIN

Query Match      16.4%; Score 628.8; DB 14; Length 646;
Best Local Similarity 99.4%; Pred. No. 4.5e-80;
Matches 642; Conservative 0; Mismatches 2; Indels 2; Gaps 1;

QY      3177 TCTTGCTGTATTTGGGGAATTGCAAAGAAAGTGGAGCTGACAGAAATAACCCCTTTTCACA 3236
      |||
Db      1 TCTTGCTGTATTTGGGGAATTGCAAAGAAAGTGGAGCTGACAGAAATAACCCCTTTTCACA 60

QY      3237 GTTTGTGCACTGTGTACGGTCTGTGTAGGTTGATGCAGATTTTCTGAAATGAAATGTTTA 3296
      |||
Db      61 GTTTGTGCACTGTGTACGGTCTGTGTAGGTTGATGCAGATTTTCTGAAATGAAATGTTTA 120

QY      3297 GACGAGATCATGCCACCAAGGCAGGAGTGAAAAAGCTTGCCTTTCTGGTATGTTCTAGG 3356
      |||
Db      121 GACGAGATCATGCCACCAAGGCAGGAGTGAAAAAGCTTGCCTTTCTGGTATGTTCTAGG 180

QY      3357 TGTATTGTGAAATTTACTGTTGTATTAATTGCCAATATAAGTAAATATAGAT--TATATA 3414
      |||
Db      181 TGTATTGTGAAATTTACTGTTGTATTAATTGCCAATATAAGTAAATATAGATTATATATA 240

QY      3415 TATCTATATATAGTGTTCACGAAGCTTAGCCCTTTACCTTCCCAGCTGCCCCACAGTGC 3474
      |||
Db      241 TATCTATATATAGTGTTCATGAAGCTTAGCCCTTTACCTTCCCAGCTGCCCCACAGTGC 300

QY      3475 TTGATACTTCTGTGCATGGGTTTTATGTGTGTAGTCCCAAAGCACATAAGCTAGGGAGAAA 3534
      |||
Db      301 TTGATACTTCTGTGCATGGGTTTTATGTGTGTAGTCCCAAAGCACATAAGCTAGGGAGAAA 360

QY      3535 CGTACTTCTAGGCGCACTACCATCTGTTTTCAACACGAACCGACGCCATGCAACAGAAC 3594
      |||
Db      361 CGTACTTCTAGGCGCACTACCATCTGTTTTCAACACGAACCGACGCCATGCAACAGAAC 420

QY      3595 TCCTCAACATAAACTTCACTGCACAGACTTACTGTAGTTAATTTTATCAGAACTCTGGA 3654
      |||
Db      421 TCCTCAACATAAACTTCACTGCACAGACTTACTGTAGTTAATTTTATCAGAACTCTGGA 480

QY      3655 CTGAATCTAATGCTTCCAAAAATGTTTGCAAATATCAAACATTGTTATGTAAGAAAATAT 3714
      |||
Db      481 CTGAATCTAATGCTTCCAAAAATGTTTGCAAATATCAAACATTGTTATGTAAGAAAATAT 540

QY      3715 AAATGACGATTTATACAATTGTGGTTTAAGCTGTATTGAACTAAATCTGTGGAATGCATT 3774
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Db 541 AAATGACGATTATACAATTGTGGTTTAAAGCTGTATTGAACTAAATCTGTGGAATGCATT 600

Qy 3775 GTGAACTGTAAAAGCAAAGTATCAATAAAGCTTATAGACTTAAAAA 3820

|||||
Db 601 GTGAACTGTAAAAGCAAAGTATCAATAAAGCTTATAGACCTAAAAA 646

RESULT 8

BM986175

LOCUS BM986175 627 bp mRNA linear EST 22-MAR-2002

DEFINITION LM24HW00149 Bos taurus LM-24-HW cDNA library Bos taurus cDNA clone
LM-24-HW-001-49 (5'), mRNA sequence.

ACCESSION BM986175

VERSION BM986175.1 GI:19684841

KEYWORDS EST.

SOURCE Bos taurus (cow)

ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 627)

AUTHORS Yoon,D.H., Jang,Y.S., Kim,T.H., Park,E.W., Lee,H.K., Chung,E.R.,
Sun,S.S. and Cheong,I.C.

TITLE Gene Expression Profiling of the Bovine skeletal muscle

JOURNAL Unpublished

COMMENT Contact: Dr. Du-Hak Yoon

National Livestock Research Institute, RDA

564 Omockchun-dong, Suwon, 441-350, Korea

Tel: 82 31 290 1593

Fax: 82 31 290 1792

Email: dhyoon@rda.go.kr

Insert Length: 839 Std Error: 0.00

Seq primer: CAGGAAACAGCTATGAC

POLYA=No.

FEATURES Location/Qualifiers

source

1..627

/organism="Bos taurus"

/mol_type="mRNA"

/db_xref="taxon:9913"

/clone="LM-24-HW-001-49 (5')"

/sex="six males mixed"

/tissue_type="longissimus dorsi"

/cell_type="myocyte"

/dev_stage="24 months old"

/lab_host="XL1-BlueMRF'strain"

/clone_lib="Bos taurus LM-24-HW cDNA library"

/note="Organ: skeletal muscle; Vector: Uni-ZAPXR; Site_1:

EcoRI; Site_2: Xho I"

BASE COUNT 191 a 95 c 148 g 193 t

ORIGIN

Query Match 16.3%; Score 625.4; DB 12; Length 627;

Best Local Similarity 99.8%; Pred. No. 1.4e-79;

Matches 626; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2766 CAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCT 2825

|||||


```

Db          1 CAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCT 60
Qy          2826 AAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGAGAAAGCCTGAAAGAG 2885
          |||
Db          61 AAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGAGAAAGCCTGAAAGAG 120
Qy          2886 TTAACAATAGAGGAGTTTATCTTTAAAGGGGATATTCATTTGATTCCATTGGGGAGGGTC 2945
          |||
Db          121 TTAACAATAGAGGAGTTTATCTTTAAAGGGGATATTCATTTGATTCCATTGGGGAGGGTC 180
Qy          2946 AGGGAAGAACAAAGCCTTGACATTGCAGTGCAGTTTCACAGATCTTTATTTTTAGCAACG 3005
          |||
Db          181 AGGGAAGAACAAAGCCTTGACATTGCAGTGCAGTTTCACAGATCTTTATTTTTAGCAACG 240
Qy          3006 CAGTGTCTGAGGAAAAATGACCTGTCTTGAAGTGCCTGTGTTTCATCATCTTAAGTATTGT 3065
          |||
Db          241 CAGTGTCTGAGGAAAAATGACCTGTCTTGAAGTGCCTGTGTTTCATCATCTTAAGTATTGT 300
Qy          3066 AAGCTGCTATGTATGGATTTAAATCGTAATCATATTTGTTTTCTGTATGAGGCACTGG 3125
          |||
Db          301 AAGCTGCTATGTATGGATTTAAATCGTAATCATATTTGTTTTCTGTATGAGGCACTGG 360
Qy          3126 TGAATAAACAAAGATCTGAGAAAGCTGTATATTACACTTTGTTCGAGGTAGTCTTGCTGT 3185
          |||
Db          361 TGAATAAACAAAGATCTGAGAAAGCTGTATATTACACTTTGTTCGAGGTAGTCTTGCTGT 420
Qy          3186 ATTTGGGGAATTGCAAAGAAAGTGGAGCTGACAGAAATAACCCTTTTCACAGTTTGTGCA 3245
          |||
Db          421 ATTTGGGGAATTGCAAAGAAAGTGGAGCTGACAGAAATAACCCTTTTCACAGTTTGTGCA 480
Qy          3246 CTGTGTACGGTCTGTGTAGGTTGATGCAGATTTTCTGAAATGAAATGTTTAGACGAGATC 3305
          |||
Db          481 CTGTGTACGGTCTGTGTAGGTTGATGCAGATTTTCTGAAATGAAATGTTTAGACGAGATC 540
Qy          3306 ATGCCACCAAGGCAGGAGTGAAAAAGCTTGCCTTTCCTGGTATGTTCTAGGTGTATTGTG 3365
          |||
Db          541 ATGCCACCAAGGCAGGAGTGAAAAAGCTTGCCTTTCCTGGTATGTTCTAGGTGTATTGTG 600
Qy          3366 AAATTTACTGTTGTATTAATTGCCAAT 3392
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Db          601 AAAATTACTGTTGTATTAATTGCCAAT 627

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RESULT 9

BG570231

LOCUS BG570231 843 bp mRNA linear EST 10-APR-2001

DEFINITION 602590632F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4717662 5', mRNA sequence.

ACCESSION BG570231

VERSION BG570231.1 GI:13577884

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 843)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: CLONTECH Laboratories, Inc.
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLCM1567 row: o column: 07
 High quality sequence stop: 801.

FEATURES Location/Qualifiers
 source 1. .843
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4717662"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NIH_MGC_77"
 /note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1:
 SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc); 5' and
 3' adaptors were used in cloning as follows: 5' adaptor
 sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
 5'-ATTCTAGAGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size 1.9
 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech Laboratories (Palo Alto,
 CA). Note: this is a NIH_MGC Library."

BASE COUNT 224 a 158 c 194 g 267 t
 ORIGIN

Query Match 16.2%; Score 621.4; DB 10; Length 843;
 Best Local Similarity 87.6%; Pred. No. 4.7e-79;
 Matches 742; Conservative 0; Mismatches 86; Indels 19; Gaps 5;

Qy 2304 GTTGTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGC 2363
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 Db 2 GTTGTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGC 61

Qy 2364 TTGTTCTGCTGCTCTCGCTGACAGTATTCAGCATTGTGAGTGTAACGGCCTACATTGCC 2423
 |
 Db 62 CTATTCTGCTGCTTTTCATTGACAGTATTCAGCATTGTGAGCGTAACAGCCTACATTGCC 121

Qy 2424 TTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAGGCTATC 2483
 |||
 Db 122 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC 181

Qy 2484 CAGAAATCTGATGAAGGCCACCCATTTCAGGGCATATTTGGAATCTGAAGTTGCTATATCT 2543
 |||
 Db 182 CAGAAATCAGATGAAGGCCACCCATTTCAGGGCATATCTGGAATCTGAAGTTGCTATATCT 241

Qy 2544 GAGGAGTTGGTTCAGAAGTACAGCAATTCTGCTCTTGGTCATGTTAACTGCACAATAAAA 2603
 |||
 Db 242 GAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAAGTGCACGATAAAG 301

Qy	2604	GAAGTCAGACGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAAGTGTG	2663
Db	302	GAAGTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAAGTGTG	361
Qy	2664	ATGTGGGTATTTACCTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTAATTTTGGCT	2723
Db	362	ATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAAATGGTCTGACACTACTGATTTTGGCT	421
Qy	2724	CTGATTTCACTCTTCAGTGTTCTGTTATTTATGAACGGCATCAGGCGCAAATAGATCAT	2783
Db	422	CTCATTTCACTCTTCAGTGTTCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT	481
Qy	2784	TATCTGGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATC	2843
Db	482	TATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATC	541
Qy	2844	CCTGGATTGAAGCGTAAAGCTGAATGAGAAAGCCTGAAAGAGTTAACAATAGAGGAGTTT	2903
Db	542	CCTGGATTGAAGCGCAAAGCTGAATGAAAACGCCCAAATAATTA-----GTAGGAGTTC	596
Qy	2904	ATCTTTAAAGGGGATATTCATTTGATTCCATTGGGGAGGGTCAGGGAAGAACAAGCCTT	2963
Db	597	ATCTTTAAAGGGGATATCCATTTGATTATACGGGGGAGGGTCAGGAAGAACAAGCCTTG	656
Qy	2964	GACATTGCAGTGCAGTTTCACAGAT-----CTTTATTTTGTAGCAACGCAGTG-T	3011
Db	657	ACGTTTGCAGTGCAGTTTCACAGATCGTAGTAGATCCTTTATTTTGTAGCCCTGCACTGTT	716
Qy	3012	CTGAGGAAAAATGACCTGTCTTGAAGT-GCCCTGTGTTTCATCATCTTAA-GTATTGTAAGC	3069
Db	717	GTGCAGGAAAAATTACCTGTCTTGAAGTGGCCATGTTGTTCATCATCTTAAAGTATTGTAAGC	776
Qy	3070	TGCTATGTATGGATTTAAATCGTAATCATATTTGTTTTCTCTGTATGAGGCACTGGTGAA	3129
Db	777	TGCTATGTATGGATTTAAACCGTATCATATCTTTTCTCTATCTAATCTGAGGACTGTGGAA	836
Qy	3130	TAAACAA	3136
Db	837	TTAAAAA	843

RESULT 10

BF044381

LOCUS BF044381 631 bp mRNA linear EST 10-OCT-2000

DEFINITION BP250021B10D3 Soares normalized bovine placenta Bos taurus cDNA clone BP250021B10D3 5', mRNA sequence.

ACCESSION BF044381

VERSION BF044381.1 GI:10761508

KEYWORDS EST.

SOURCE Bos taurus (cow)

ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 631)

AUTHORS Lewin,H.A., Soares,M.B., Rebeiz,M., Pardinas,J., Liu,L. and Larson

,J.H.
 TITLE Bovine ESTs
 JOURNAL Unpublished
 COMMENT Contact: Lewin, H. A.
 W. M. Keck Center for Comparative and Functional Genomics
 University of Illinois at Urbana-Champaign
 340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL
 61801, USA
 Tel: 217 333 5998
 Fax: 217 244 5617
 Email: h-lewin@uiuc.edu
 Funding for cattle EST sequencing was provided by the USDA National
 Research Initiative, Animal Genome Resource Grant AG 99-3205-8534
 to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED
 from Washington University Genome Center. Vector Trimmi g:
 Cross_match from Washington University Genome Center PHRAP suite.
 This sequence is vector free and at least 200 bp in length.
 PCR Primers
 FORWARD: TAATACGACTCACTATAGGG
 BACKWARD: ATTAACCCTCACTAAAG
 Insert Length: 631 Std Error: 0.00
 Plate: BP250021B10 row: D column: 3
 Seq primer: AGCGGATAACAATTTACACAGGA
 High quality sequence stop: 631.

FEATURES Location/Qualifiers
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 /organism="Bos taurus"
 /mol_type="mRNA"
 /db_xref="taxon:9913"
 /clone="BP250021B10D3"
 /sex="female"
 /lab_host="DH10B"
 /clone_lib="Soares normalized bovine placenta"
 /note="Organ: placenta; Vector: pT7T3Pac; Site_1: EcoRI;
 Site_2: NotI; The cDNA library was contributed by the
 Soares laboratory and it was constructed and normalized
 as described by Bonaldo, M.F., Lennon, G. and Soares,
 M.B. (1996), Genome Research 6(9): 791-806. "

BASE COUNT 188 a 97 c 142 g 204 t
 ORIGIN

Query Match 16.1%; Score 617; DB 10; Length 631;
 Best Local Similarity 99.7%; Pred. No. 2.2e-78;
 Matches 629; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

Qy 2834 AGCAAAATCCCTGGATTGAAGCGTAAAGCTGAATGAGAAAGCCTGAAAGAGTTAACAAT 2893
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 AGCAAAATCCCTGGATTGAAGCGTAAAGCTGAATGAGAAAGCCTGAAAGAGTTAACAAT 60
 Qy 2894 AGAGGAGTTTATCTTTAAAGGGGATATTCATTTGATTCCATTGGGGAGGGTCAGGGAAGA 2953
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 AGAGGAGTTTATCTTTAAAGGGGATATTCATTTGATTCCATTGGGGAGGGTCAGGGAAGA 120
 Qy 2954 ACAAAGCCTTGACATTGCAGTGCAGTTTCACAGATCTTTATTTTATAGCAACGCAGTGTCT 3013
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 121 ACAAAGCCTTGACATTGCAGTGCAGTTTCACAGATCTTTATTTTATAGCAACGCAGTGTCT 180

Qy 3014 GAGGAAAAATGACCTGTCTTGACTGCCCTGTGTTTCATCATCTTAAGTATTGTAAGCTGCT 3073
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 181 GAGGAAAAATGACCTGTCTTGACTGCCCTGTGTTTCATCATCTTAAGTATTGTAAGCTGCT 240

Qy 3074 ATGTATGGATTTAAATCGTAATCATATTTGTTTTTCCTGTATGAGGCACTGGTGAATAAA 3133
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 Db 241 ATGTATGGATTTAAATCGTAATCATATTTGTTTTTCCTGTATGAGGCACTGGTGAATAAA 300

Qy 3134 CAAAGATCTGAGAAAGCTGTATATTACACTTTGTCGCAGGTAGTCTTGCTGTATTTGGGG 3193
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 301 CAAAGATCTGAGAAAGCTGTATATTACACTTTGTCGCAGGTAGTCTTGCTGTATTTGGGG 360

Qy 3194 AATTGCAAAGAAAGTGGAGCTGACAGAAATAACCCCTTTTCACAGTTTGTGCACTGTGTAC 3253
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 361 AATTGCAAAGAAAGTGGAGCTGACAGAAATAACCCCTTTTCACAGTTTGTGCACTGTGTAC 420

Qy 3254 GGTCTGTGTAGGTTGATGCAGATTTTCTGAAATGAAATGTTTAGACGAGATCATGCCACC 3313
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 421 GGTCTGTGTAGGTTGATGCAGATTTTCTGAAATGAAATGTTTAGACGAGATCATGCCACC 480

Qy 3314 AAGGCAGGAGTGAAAAAGCTTGCCTTTTCCTGGTATGTTCTAGGTGTATTGTGAAATTTAC 3373
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 481 AAGGCAGGAGTGAAAAAGCTTGCCTTTTCCTGGTATGTTCTAGGTGTATTGTGAAATTTAC 540

Qy 3374 TGTGTATTAAATTGCCAATATAAGTAAATATAGAT--TATATATATCTATATATAGTGTT 3431
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 541 TGTGTATTAAATTGCCAATATAAGTAAATATAGATTATATATATATCTATATATAGTGTT 600

Qy 3432 TCACGAAGCTTAGCCCTTTACCTTCCCAGCT 3462
 ||||||||||||||||||||||||||||||||||||
 Db 601 TCACGAAGCTTAGCCCTTTACCTTCCCAGCT 631

RESULT 11
 CB521332

LOCUS CB521332 822 bp mRNA linear EST 28-MAR-2003
 DEFINITION UI-M-GH0-cem-h-13-0-UI.r1 NIH_BMAP_GH0 Mus musculus cDNA clone
 IMAGE: 6841502 5', mRNA sequence.

ACCESSION CB521332
 VERSION CB521332.1 GI:29354687
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 822)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Dr. Jim Lin, University of Iowa
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/mousefl.html>


```

      ||| ||||| ||||||||| ||| ||||||||| ||| ||||||||| |||||
Db      289 GCAACATAGTTAAACCCAAAGTACTTACGAAAGAAGCAGAGGAAAAACTTCC'TTCTGATA 348
Qy      2245 CAGAAAAAGAGCGAAGATCTCCATCTGCTATATTTTCAGCAGAGCTGAGTAAAC'TTCAG 2304
      ||||| ||||| ||||| | ||| ||||| ||||||||| ||||||||| |||||
Db      349 CAGAGAAAGAGGACAGATCCCTGACAGCTGTATTGTCAGCAGAGCTGAATAAAACTTCAG 408
Qy      2305 TTGTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGT'TTGGTGCCAGCT 2364
      ||||||||| ||||||||| ||||||||| ||||||||| ||||||||| ||||||||| |||||
Db      409 TTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGT'TTGGTGCCAGCT 468
Qy      2365 TGTTCCCTGCTGCTCTCGCTGACAGTATTTCAGCATTGTGAGTGTAAACGGCCTACATTGCCT 2424
      | ||||||||| || ||||||||| || ||||||| ||||||||| ||||||||| |||||
Db      469 TATTCCTGCTGCTGTCTCTGACAGTGTT--TCATTGTCAGTGTAAACGGCCTACATTGCCT 526
Qy      2425 TGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAGGCTATCC 2484
      ||||||||| ||||||||| ||||||||| ||||||||| ||||||||| ||||||||| |||||
Db      527 TGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAAGCTATCC 586
Qy      2485 AGAAATCTGATGAAGGCCACCCATTTCAGGGCATATTTGGAATCTGAAGTTGCTATATCTG 2544
      ||||||| ||||||||| ||||||||| ||||||||| ||||||||| ||||||||| |||||
Db      587 AGAAATCAGATGAAGGCCACCCATTTCAGGGCATATTTGGAATCTGAAGTTGCCATATCAG 646
Qy      2545 AGGAGTTGGTTTCAGAAGTACAGCAATTCTGCTCTTGGTCATGTTAAGTGCACAATAAAAG 2604
      ||||| ||||||||| || || ||||||||| || ||||||||| || ||||||||| |||||
Db      647 AGGAATTGGTTTCAGAAATATAGTAATTCTGCTCTTGGTCATGTGAACAGCACATAAAAG 706
Qy      2605 AACTCAGACGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGT'TGA 2664
      || | || || ||||||||| ||||||||| ||||||||| ||||||||| ||||||||| |||||
Db      707 AATTGAGGCGTCTCTTCTTAGTTGATGACTTAGTTGATTCCCTGAAGTTTGCAGTGT'TGA 766
Qy      2665 TGTGGGTATTTACCTATGTTGGTGCCTTGTTCATGGTCTGACACTACTAATTTT 2719
      ||||||||| || ||||||||| ||||||||| ||||||||| || |||||
Db      767 TGTGGGTATTTACTTACGTTGGTGCCTTGTTCATGGTTTGACACTACTGACTTT 821

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RESULT 12

BQ879359

LOCUS BQ879359 901 bp mRNA linear EST 16-AUG-2002

DEFINITION AGENCOURT_8119868 Lupski_dorsal_root_ganglion Homo sapiens cDNA clone IMAGE:6177832 5', mRNA sequence.

ACCESSION BQ879359

VERSION BQ879359.1 GI:22271367

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 901)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. James R. Lupski

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLAM13556 row: g column: 17
 High quality sequence stop: 609.

FEATURES
 source Location/Qualifiers
 1. .901
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6177832"
 /sex="male"
 /tissue_type="dorsal root ganglia"
 /dev_stage="adult, 36 yr"
 /lab_host="DH10B"
 /clone_lib="Lupski_dorsal_root_ganglion"
 /note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
 NotI; Site_2: SalI; cDNA made by oligo-dT priming.
 Directionally cloned using the following adaptors:
 5'-TCGACCCACGCGTCCG-3' and
 5'-GACTAGTTCTAGATCGCGAGCGGCCCCCT(15)-3'. Size selected >
 1 kb for average insert length 1.7 kb. This is a primary
 library, non-amplified. Library constructed by Life
 Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
 College of Medicine) and is available through Life
 Technologies."

BASE COUNT 246 a 161 c 203 g 291 t
 ORIGIN

Query Match 15.8%; Score 605.2; DB 13; Length 901;
 Best Local Similarity 86.6%; Pred. No. 9.3e-77;
 Matches 783; Conservative 0; Mismatches 83; Indels 38; Gaps 9;

Qy 2413 CCTACATTGCCTTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGA 2472
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 Db 1 CCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATA-CAGGGTGTGA 59
 Qy 2473 TCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATTTCAGGGCATATTTGGAATCTGAAG 2532
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 Db 60 TCCAAGCTATCCAGAAATCATATGAAGGCCACCCATTTCAGGGCATATCTGGAATCTGAAG 119
 Qy 2533 TTGCTATATCTGAGGAGTTGGTTTCAGAAGTACAGCAATTCTGCTCTTGGTCATGTAACT 2592
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 Db 120 TTGCTATATCTGAGGAGTTGGTTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTAACT 179
 Qy 2593 GCACAATAAAAGAACTCAGACGCCTCTTCTTAGTTGATGATTAGTTGATTCTCTGAAGT 2652
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 Db 180 GCACGATAAAGGAACTCAGCGCCTCTTCTTAGTTGATGATTAGTTGATTCTCTGAAGT 239
 Qy 2653 TTGCAGTGTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTCATGGTCTGACACTAC 2712
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 Db 240 TTGCAGTGTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTCTGACACTAC 299
 Qy 2713 TAATTTTGGCTCTGATTTCACTCTTCAGTGTTCCCTGTTATTTATGAACGGCATCAGGCGC 2772
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 Db 300 TGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCCTGTTATTTATGAACGGCATCAGGCAC 359

,J.H.
 TITLE Bovine ESTs
 JOURNAL Unpublished
 COMMENT Contact: Lewin, H. A.
 W. M. Keck Center for Comparative and Functional Genomics
 University of Illinois at Urbana-Champaign
 340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL
 61801, USA
 Tel: 217 333 5998
 Fax: 217 244 5617
 Email: h-lewin@uiuc.edu
 Funding for cattle EST sequencing was provided by the USDA National
 Research Initiative, Animal Genome Resource Grant AG 99-3205-8534
 to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED
 from Washington University Genome Center. Vector Trimmi g:
 Cross_match from Washington University Genome Center PHRAP suite.
 This sequence is vector free and at least 200 bp in length.
 PCR Primers
 FORWARD: TAATACGACTCACTATAGGG
 BACKWARD: ATTAACCCTCACTAAAG
 Insert Length: 593 Std Error: 0.00
 Plate: BP250015A10 row: C column: 2
 Seq primer: AGCGGATAACAATTTACACAGGA
 High quality sequence stop: 593.

FEATURES
 source Location/Qualifiers
 1. .593
 /organism="Bos taurus"
 /mol_type="mRNA"
 /db_xref="taxon:9913"
 /clone="BP250015A10C2"
 /sex="female"
 /lab_host="DH10B"
 /clone_lib="Soares normalized bovine placenta"
 /note="Organ: placenta; Vector: pT7T3Pac; Site_1: EcoRI;
 Site_2: NotI; The cDNA library was contributed by the
 Soares laboratory and it was constructed and normalized
 as described by Bonaldo, M.F., Lennon, G. and Soares,
 M.B. (1996), Genome Research 6(9): 791-806. "

BASE COUNT 167 a 100 c 136 g 190 t
 ORIGIN

Query Match 15.4%; Score 591.4; DB 10; Length 593;
 Best Local Similarity 99.8%; Pred. No. 9.8e-75;
 Matches 592; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2488 AATCTGATGAAGGCCACCCATTTCAGGGCATATTTGGAATCTGAAGTTGCTATATCTGAGG 2547
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 Db 1 AATCTGATGAAGGCCACCCATTTCAGGGCATATTTGGAATCTGAAGTTGCTATATCTGAGG 60
 Qy 2548 AGTTGGTTTCAGAAGTACAGCAATTCTGCTCTTGGTCATGTTAACTGCACAATAAAAGAAC 2607
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 Db 61 AGTTGGTTTCAGAAGTACAGCAATTCTGCTCTTGGTCATGTTAACTGCACAATAAAAGAAC 120
 Qy 2608 TCAGACGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTGATGT 2667
 |||
 Db 121 TCAGACGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTGATGT 180

Qy 2668 GGGTATTTACCTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTAATTTTGGCTCTGA 2727
 |||
 Db 181 GGGTATTTACCTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTAATTTTGGCTCTGA 240
 Qy 2728 TTTCACCTCTTCAGTGTTCTGTATTTATGAACGGCATCAGGCGCAAATAGATCATTATC 2787
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 Db 241 TTTCACCTCTTCAGTGTTCTGTATTTATGAACGGCATCAGGCGCAAATAGATCATTATC 300
 Qy 2788 TGGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTG 2847
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 Db 301 TGGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTG 360
 Qy 2848 GATTGAAGCGTAAAGCTGAATGAGAAAGCCTGAAAGAGTTAACAATAGAGGAGTTTATCT 2907
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 Db 361 GATTGAAGCGTAAAGCTGAATGAGAAAGCCTGAAAGAGTTAACAATAGAGGAGTTTATCT 420
 Qy 2908 TTAAAGGGGATATTTCATTTGATTCCATTGGGGAGGGTCAGGGAAGAACAAGCCTTGACA 2967
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 Db 421 TTAAAGGGGATATTTCATTTGATTCCATTGGGGAGGGTCAGGGAAGAACAAGCCTTGACA 480
 Qy 2968 TTGCAGTGCAGTTTCACAGATCTTTATTTTGTAGCAACGCAGTGTCTGAGGAAAAATGACC 3027
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 Db 481 TTGCAGTGCAGTTTCACAGATCTTTGTTTTGTAGCAACGCAGTGTCTGAGGAAAAATGACC 540
 Qy 3028 TGTCTTGACTGCCCTGTGTTTCATCATCTTAAGTATTGTAAGCTGCTATGTATG 3080
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 Db 541 TGTCTTGACTGCCCTGTGTTTCATCATCTTAAGTATTGTAAGCTGCTATGTATG 593

RESULT 14

BI775114

LOCUS BI775114 587 bp mRNA linear EST 25-SEP-2001

DEFINITION 467491 MARC 1BOV Bos taurus cDNA 5', mRNA sequence.

ACCESSION BI775114

VERSION BI775114.1 GI:15776091

KEYWORDS EST.

SOURCE Bos taurus (cow)

ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 587)

AUTHORS Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
 Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett
 ,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G.,
 Perteau,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and
 Keele,J.W.

TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA
 libraries and construction of a gene index for cattle

JOURNAL Genome Res. 11 (4), 626-630 (2001)

MEDLINE 21180013

PUBMED 11282978

COMMENT Contact: Smith TPL

USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390

Email: smith@email.marc.usda.gov
 Single pass sequencing. Bases called and alt_trimmed with phred
 v0.980904.e. Vector identified by cross_match with the -minscore 18
 and -minmatch 12 options.
 PCR Primers
 FORWARD: AGGAAACAGCTATGACCAT
 BACKWARD: GTTTTCCCAGTCACGACG
 Plate: 144 row: C column: 22
 Seq primer: ATTTAGGTGACACTATAG.

FEATURES	Location/Qualifiers
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	/organism="Bos taurus"
	/mol_type="mRNA"
	/db_xref="taxon:9913"
	/tissue_type="pooled"
	/lab_host="DH10B"
	/clone_lib="MARC 1BOV"
	/note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI; Library made from pooled tissue from lymph node, ovary, fat, hypothalamus, and pituitary."

BASE COUNT 166 a 103 c 134 g 184 t
 ORIGIN

Query Match 15.3%; Score 587; DB 12; Length 587;
 Best Local Similarity 100.0%; Pred. No. 4.2e-74;
 Matches 587; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	2469	GTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATT	CAGGGCATATTTGGAATCT	2528
Db	1	GTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATT	CAGGGCATATTTGGAATCT	60
Qy	2529	GAAGTTGCTATATCTGAGGAGTTGGTT	CAGAAGTACAGCAATTCTGCTCTTG	2588
Db	61	GAAGTTGCTATATCTGAGGAGTTGGTT	CAGAAGTACAGCAATTCTGCTCTTG	120
Qy	2589	AACTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTG		2648
Db	121	AACTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTG		180
Qy	2649	AAGTTTGCACTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTCAATGGTCTGACA		2708
Db	181	AAGTTTGCACTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTCAATGGTCTGACA		240
Qy	2709	CTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCCCTGTTATTTATGAACGGCATCAG		2768
Db	241	CTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCCCTGTTATTTATGAACGGCATCAG		300
Qy	2769	GCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAA		2828
Db	301	GCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAA		360
Qy	2829	ATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGAGAAAGCCTGAAAGAGTTA		2888
Db	361	ATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGAGAAAGCCTGAAAGAGTTA		420
Qy	2889	ACAATAGAGGAGTTTATCTTTAAAGGGGATATTCATTTGATTCCATTGGGGAGGGTCAGG		2948

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Db      421 ACAATAGAGGAGTTTATCTTTAAAGGGGATATTCATTTGATTCCATTGGGGAGGGTCAGG 480
Qy      2949 GAAGAACAAAGCCTTGACATTGCAGTGCAGTTTTCACAGATCTTTATTTTTCAGCAACGCAG 3008
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 GAAGAACAAAGCCTTGACATTGCAGTGCAGTTTTCACAGATCTTTATTTTTCAGCAACGCAG 540
Qy      3009 TGTCTGAGGAAAAATGACCTGTCTTGACTGCCCTGTGTTCATCATCT 3055
        ||||||||||||||||||||||||||||||||||
Db      541 TGTCTGAGGAAAAATGACCTGTCTTGACTGCCCTGTGTTCATCATCT 587

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RESULT 15

BM801698

LOCUS BM801698 958 bp mRNA linear EST 05-MAR-2002

DEFINITION AGENCOURT_6458941 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:5558493
5', mRNA sequence.

ACCESSION BM801698

VERSION BM801698.1 GI:19118521

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 958)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM12281 row: i column: 22

High quality sequence start: 25

High quality sequence stop: 579.

FEATURES

source

Location/Qualifiers

1. .958

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5558493"

/tissue_type="duodenal adenocarcinoma, cell line"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_88"

/note="Organ: small intestine; Vector: pCMV-SPORT6;

Site_1: NotI; Site_2: SalI; Cloned unidirectionally;

oligo-dT primed. Average insert size 1.767 kb. Library
enriched for full-length clones and constructed by Life

Technologies. Note: this is a NIH_MGC Library."

BASE COUNT 247 a 215 c 218 g 278 t

ORIGIN

Query Match

15.2%; Score 581.2; DB 12; Length 958;

Best Local Similarity 91.5%; Pred. No. 2.4e-73;
Matches 639; Conservative 0; Mismatches 53; Indels 6; Gaps 2;

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Qy      2304 GTTGTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGC 2363
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Db      66 GTTGTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGC 125

Qy      2364 TTGTTCCCTGCTGCTCTCGCTGACAGTATTCAGCATTGTGAGTGTAACGGCCTACATTGCC 2423
          |
Db      126 CTATTCCCTGCTGCTTTTCATTGACAGTATTCAGCATTGTGAGCGTAACAGCCTACATTGCC 185

Qy      2424 TTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAGGCTATC 2483
          |||
Db      186 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC 245

Qy      2484 CAGAAATCTGATGAAGGCCACCCATTTCAGGGCATATTTGGAATCTGAAGTTGCTATATCT 2543
          |||
Db      246 CAGAAATCAGATGAAGGCCACCCATTTCAGGGCATATCTGGAATCTGAAGTTGCTATATCT 305

Qy      2544 GAGGAGTTGGTTCAGAAGTACAGCAATTCTGCTCTTGGTCATGTAACTGCACAATAAAA 2603
          |||
Db      306 GAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAACTGCACGATAAAG 365

Qy      2604 GAACTCAGACGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTG 2663
          |||
Db      366 GAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTG 425

Qy      2664 ATGTGGGTATTTACCTATGTTGGTGCCTTGTTCATGGTCTGACACTACTAATTTTGGCT 2723
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Db      426 ATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTCTGACACTACTGATTTTGGCT 485

Qy      2724 CTGATTTCACTCTTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCGCAAATAGATCAT 2783
          ||
Db      486 CTCATTTCACTCTTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT 545

Qy      2784 TATCTGGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATC 2843
          |||
Db      546 TATCTACGACTTGCAAATAAGAATGCTAAAGATGCTATGGCTAAAATCCAAGCAAAAATC 605

Qy      2844 CCTGGATTGAAGCGTAAAGCTGAATGAGAAAGCCTGAAAGAGTTAACAATAGAGGAGTTT 2903
          |||
Db      606 CCTGGATTGAAGCGCAAAGCTGAATGAAAACGCCAAAATAATTA-----GTACGAGTTC 660

Qy      2904 ATCTTTAAAGGGGATATTCATTTGATTCCATTGGGGAGGGTCAGGGAAGAACAAGCCTT 2963
          |||
Db      661 CTCTTTAAAGGGGATATTCATTTGATTATACGGGGAGGGTCAGGCAAGAACGAA-CCTT 719

Qy      2964 GACATTGCAGTGCAGTTTCACAGATCTTTATTTTAGC 3001
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Db      720 GACGTTGCAGTGCAGTTTCACAAATCGCTGGTTAGATC 757

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Job time : 7424.52 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 23, 2004, 00:42:43 ; Search time 918.523 Seconds
(without alignments)
11264.762 Million cell updates/sec

Title: US-09-830-972-28
Perfect score: 3833
Sequence: 1 ctatctctctctctcagccgc.....ttaaaaaaaaaaaaaaaaaaaaaa 3833

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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24: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*
25: /SIDS1/gcgdata/ eseqn-embl/NA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match Length	DB	ID	Description
	1	3833	100.0	3833	21	AAD01174
	2	2687.8	70.1	4822	24	ABS70449
	3	2649.8	69.1	4632	24	ABV94680
	4	2566.4	67.0	4698	25	ABX34563
	5	2379.4	62.1	4053	22	AAS09453
	6	2370.4	61.8	4093	21	AAA23454
	7	2223.6	58.0	CTG3579	21	AAZ56886
	8	2223.6	58.0	3579	22	AAF90324
	9	2223.6	58.0	3579	24	ABN86601
	10	2223.6	58.0	3579	24	ABK90134
	11	2183.4	57.0	4684	21	AAD01173
	12	2179.4	56.9	4684	24	ABN86600
	13	1777.2	46.4	2386	19	AAV30920
	14	1774	46.3	2386	22	AAF98399
	15	1414.6	36.9	1980	22	AAI98079
c	16	1039.8	27.1	1758	22	AAF32725
	17	1031.8	26.9	2240	21	AAC64406
	18	1025.4	26.8	2235	24	ABV94681
	19	989.2	25.8	1514	24	ABK34580
	20	986	25.7	1798	24	ABK90135
	21	827.2	21.6	2052	24	ABK90133
	22	750.4	19.6	1568	21	AAD01175
	23	685.8	17.9	1213	20	AAX04379
	24	685.8	17.9	1610	21	AAZ36230
	25	681.4	17.8	991	20	AAX97587
	26	681.2	17.8	1694	22	AAK94408
	27	590.8	15.4	799	19	AAV23695
	28	573.4	15.0	770	21	AAA72983
	29	573.4	15.0	1216	24	ABA05903
	30	539	14.1	1683	22	AAD0
	31	538.8	14.1	868	21	AAZ56887
c	32	535	14.0	4710	22	AAL04697
c	33	535	14.0	4710	23	ABL97604
	34	527	13.7	600	22	AAF90323
	35	527	13.7	1122	21	AAZ56888
	36	527	13.7	1122	22	AAF90325
	37	464	12.1	472	25	ABX50578
	38	463.4	12.1	3535	22	AAH72837
	39	427.2	11.1	447	25	ABX50261
	40	427	11.1	441	25	ABX53872
	41	423.8	11.1	429	25	ABX53062
	43	418.8	10.9	422	25	ABX46402
c	44	413.2	10.8	742	22	AAI96236
	45	398	10.4	406	25	ABX50364

|||| ||

ALIGNMENTS

RESULT 1

AAD01174

ID AAD01174 standard; cDNA; 3833 BP.

XX

AC AAD01174;

XX

DT 02-NOV-2000 (first entry)

XX

DE Bovine neurite growth inhibitor Nogo cDNA.

XX

KW Bovine; neurite growth inhibitor; Nogo; neural cell; myelin; CNS;
 KW central nervous system; neoplastic disease; antiproliferative; glioma;
 KW antisense gene therapy; neuroblastoma; menagioma; retinoblastoma;
 KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
 KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
 KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
 KW structural plasticity; screening; ss.

XX

OS Bos sp.

XX

PN WO200031235-A2.

XX

PD 02-JUN-2000.

XX

PF 05-NOV-1999; 99WO-US26160.

XX

PR 06-NOV-1998; 98US-0107446.

XX

PA (SCHW/) SCHWAB M E.

PA (CHEN/) CH1900XT

TTGTC

XX

PI Schwab ME, Chen MS;

XX

DR WPI; 2000-400052/34.

XX

PT Nogo proteins and nucleic acids useful for treating neoplastic
 PT disorders of the central nervous system and inducing regeneration of
 PT neurons -

XX

PS Claim 26; Fig 12; 122pp; English.

XX

CC The present sequence is a cDNA encoding bovine Nogo protein which is a
 CC potent neural cell growth inhibitor and is free of all central nervous
 CC system (CNS) myelin material with which it is natively associated. The
 CC present sequence was obtained from bovine spinal cord white matter cDNA
 CC library. Nogo proteins and fragments displaying neurite growth inhibitory
 CC activity are used in the treatment of neoplastic disease of the CNS
 CC e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma, ependyoma,
 CC pinealoma, haemangioblastoma, acoustic neuroma, oligodendroglioma,
 CC menagioma, neuroblastoma, retinoblastoma and degenerative nerve TG 2745e
 CC diseases e.g. Alzheimer's and Parkinson's diseases. Therapeutics which
 CC promote Nogo activity can be used to treat or prevent hyperproliferative
 CC or benign dysproliferative disorders e.g. psoriasis and tissue
 CC hypertrophy. Ribozymes or antisense Nogo nucleic acids can be used to
 CC inhibit production of Nogo protein to induce regeneration of neurons or
 CC to promote structural plasticity of the CNS in disorders where neurite

CC growth, regeneration or maintenance are deficient or desired.
CC The animal models can be used in diagnostic and screening methods for
CC predisposition to disorders and to screen for or test molecules which
CC can treat or prevent disorders or diseases of the CNS.
CC Note: SEQ ID numbers 35-42 are referred in claim 32 and SEQ ID NO: 29
CC in disclosure of the specification. However the specification does not
CC include sequences for these SEQ ID numbers.

XX

SQ Sequence 3833 BP; 1235 A; 717 C; 818 G; 1063 T; 0 other;

Query Match 100.0%; Score 3833; DB 21; Length 3833;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3833; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	CTATCTCCTCTCTCAGCCGCTGCTTTTAAAGAACGTGAATACCTTGGTGATTTACCAGCA	60
Db	1	CTATCTCCTCTCTCAGCCGCTGCTTTTAAAGAACGTGAATACCTTGGTGATTTACCAGCA	60
Qy	61	GTACTGCCCCACTGAAGGAACACTTCCAGCAACTTCAAATGAAGCTTCTAAAGCATTCTCA	120
Db	61	GTACTGCCCCACTGAAGGAACACTTCCAGCAACTTCAAATGAAGCTTCTAAAGCATTCTCA	120
Qy	121	GAGAAGGCCAAAAATCCATTTGTAGAGAGAAATTTAACAGAATTTTCAGAATTGGAATAT	180
Db	121	GAGAAGGCCAAAAATCCATTTGTAGAGAGAAATTTAACAGAATTTTCAGAATTGGAATAT	180
Qy	181	TCAGAAATGGAATCATCATTCAGTGGCTCTCAAAAGGCAGAACCTGCCGTAACAGTAGCG	240
Db	181	TCAGAAATGGAATCATCATTCAGTGGCTCTCAAAAGGCAGAACCTGCCGTAACAGTAGCG	240
Qy	241	AATCCTAGGGACGAAATAGTTGTGAGGAGTAGAGATAAAGAAGAGGACTTAGTTAGTCTT	300
Db	241	AATCCTAGGGACGAAATAGTTGTGAGGAGTAGAGATAAAGAAGAGGACTTAGTTAGTCTT	300
Qy	301	AACATCCTTCATACTCAGCAGGAGTTATCTACAGTCCTTACGAAATCAGTTGAAGAAGAA	360
Db	301	AACATCCTTCATACTCAGCAGGAGTTATCTACAGTCCTTACGAAATCAGTTGAAGAAGAA	360
Qy	361	GATAGAGTTCTGTCTCCAGAAAAACAAAGGACAGTTTAAAGGAAAAGGGAGTTGCAGCA	420
Db	361	GATAGAGTTCTGTCTCCAGAAAAACAAAGGACAGTTTAAAGGAAAAGGGAGTTGCAGCA	420
Qy	421	GAAGCTTCTATGGGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG	480
Db	421	GAAGCTTCTATGGGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG	480
Qy	481	AAAGATACTTACAAGCAAGATAGTGATGTTTTGATTGCTGGAGGTAATATAGAGAGCAAA	540
		8 ID NOS:	
Db	481	AAAGATACTTACAAGCAAGATAGTGATGTTTTGATTGCTGGAGGTAATATAGAGAGCAAA	540
Qy	541	TTGGAAGGTAAAGTGGATAAGAAACACTTTTCAGATAGCCTTGAACAAACAAATCGTGAA	600
Db	541	TTGGAAGGTAAAGTGGATAAGAAACACTTTTCAGATAGCCTTGAACAAACAAATCGTGAA	600
Qy	601	AAAGATAGTGAAAGCAGTAATGATGACACTTCATTTCCAGTACACCAGAAGCTGTAAGA	660
Db	601	AAAGATAGTGAAAGCAGTAATGATGACACTTCATTTCCAGTACACCAGAAGCTGTAAGA	660

Qy	661	GGTGGTTCCGGAGCGTACATCACGTGTGCTCCCTTTAACCCAAACAAC	TGAGAATGTTTCA	720
Db	661	GGTGGTTCCGGAGCGTACATCACGTGTGCTCCCTTTAACCCAAACAAC	TGAGAATGTTTCA	720
Qy	721	ACAAACATTTTCCCTTGTTGGAAGATCATACTTCGGAAAATAAGACAGATGAAAAAAG		780
Db	721	ACAAACATTTTCCCTTGTTGGAAGATCATACTTCGGAAAATAAGACAGATGAAAAAAG		780
Qy	781	ATAGAAAAAAAAGGCACAAATTGTAACAGAGAAGAATGCAAGTGTCAAGACATCAAACC		840
Db	781	ATAGAAAAAAAAGGCACAAATTGTAACAGAGAAGAATGCAAGTGTCAAGACATCAAACC		840
Qy	841	CTTTCCTTATGGCAGCACAGGAGTCTAAGACAGATTACGTTACAACAGATCATGTGTCAA		900
Db	841	CTTTCCTTATGGCAGCACAGGAGTCTAAGACAGATTACGTTACAACAGATCATGTGTCAA		900
Qy	901	AGGTGACCGAGGAAGTAGTGGCAAACATGCCTGAAGGTCTAACCCCAGATTGGTTTCAGG		960
Db	901	AGGTGACCGAGGAAGTAGTGGCAAACATGCCTGAAGGTCTAACCCCAGATTGGTTTCAGG		960
Qy	961	AAGCATGTGAAAGTGAATTGAATGAAGCTACTGGTACAAAAATTGCCTTTGAAACAAAAA		1020
Db	961	AAGCATGTGAAAGTGAATTGAATGAAGCTACTGGTACAAAAATTGCCTTTGAAACAAAAA		1020
Qy	1021	TGGACCTGGTTCAAACCTCAGAAGCTGTGCAGGAGTCACTTTACCTGTAAACAGCTTT		1080
Db	1021	TGGACCTGGTTCAAACCTCAGAAGCTGTGCAGGAGTCACTTTACCTGTAAACAGCTTT		1080
Qy	1081	GCCCATCTTTTGAAGAATCTGAAGCTACTCCGTCACCGGTTTTGCCTGACATTGTCATGG		1140
Db	1081	GCCCATCTTTTGAAGAATCTGAAGCTACTCCGTCACCGGTTTTGCCTGACATTGTCATGG		1140
Qy	1141	AAGCACCATTAAATCTGTAGTTCCTAGTGCTGGTGCTTCTGCAGTGCAGCTCAGTTCAT		1200
Db	1141	AAGCACCATTAAATCTGTAGTTCCTAGTGCTGGTGCTTCTGCAGTGCAGCTCAGTTCAT		1200
Qy	1201	CACCATTAGAAACTCTTCTTCAGTTAATTATGAAAGCATAAAGTTTGAGCCTGAAAATC		1260
Db	1201	CACCATTAGAAACTCTTCTTCAGTTAATTATGAAAGCATAAAGTTTGAGCCTGAAAATC		1260
Qy	1261	CCCCACCATATGAGGAGGCCATGAATGTATCACTAAAAAAGAATCAGGAATGAATGAAG		1320
Db	1261	CCCCACCATATGAGGAGGCCATGAATGTATCACTAAAAAAGAATCAGGAATGAATGAAG		1320
Qy	1321	AAATCACAGAGCCTGAAGGTATTAGTGTAGCTGTTTCAGGAAACAGAAGCTCCTTATATAT		1380
Db	1321	AAATCACAGAGCCTGAAGGTATTAGTGTAGCTGTTTCAGGAAACAGAAGCTCCTTATATAT		1380
Qy	1381	CTATTGCATGTGATTTAATTAAAGAAACAAAGATCTCTACTGAACCGACTCCAGATTTCT		1440
Db	1381	CTATTGCATGTGATTTAATTAAAGAAACAAAGATCTCTACTGAACCGACTCCAGATTTCT		1440
Qy	1441	CTAGTTATTTCAGAAATAGCAGAAGTTGCACAGCCAGTGCCCGAGCATTCTGAGCTAGTTG		1500
Db	1441	CTAGTTATTTCAGAAATAGCAGAAGTTGCACAGCCAGTGCCCGAGCATTCTGAGCTAGTTG		1500

Qy	1501	AAGATTCTCTCCCCGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCCGAAG	1560
Db	1501	AAGATTCTCTCCCCGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCCGAAG	1560
Qy	1561	TTCCACAAAAACAAGATGAAGCTGTAATACTTGTGAAAGAAAACCTCACTGAAATTTTCAT	1620
Db	1561	TTCCACAAAAACAAGATGAAGCTGTAATACTTGTGAAAGAAAACCTCACTGAAATTTTCAT	1620
Qy	1621	CTGAGTCAATGACAGGACATGACAATAAGGGAAAACTCAGTGCTTCACCATCACCTGAGG	1680
Db	1621	CTGAGTCAATGACAGGACATGACAATAAGGGAAAACTCAGTGCTTCACCATCACCTGAGG	1680
Qy	1681	GAGGAAAACCGTATTTGGAGTCTTTTCAGCCCAGTTTAGGCATCACAAAAGATACCTTAG	1740
Db	1681	GTATTTGGAGTCTTTTCAGCCCAGTTTAGGCATCACAAAAGATACCTTAG	1740
Qy	1741	CACCTGATGAAGTTTCAGCATTGACCCAAAAGGAGAAAAATCCCTTTGCAGATGGAGGAGC	1800
Db	1741	CACCTGATGAAGTTTCAGCATTGACCCAAAAGGAGAAAAATCCCTTTGCAGATGGAGGAGC	1800
Qy	1801	TCAATACTGCAGTTTATTCAAGTGATGGCTTATTCATTGCTCAGGAAGCAAACCTAAGAG	1860
Db	1801	TCAATACTGCAGTTTATTCAAGTGATGGCTTATTCATTGCTCAGGAAGCAAACCTAAGAG	1860
Qy	1861	AAAGTGAAACATTTTCAGATTTCATCTCCGATTGAGATTATAGATGAGTTCCCGACCTTTG	1920
Db	1861	AAAGTGAAACATTTTCAGATTTCATCTCCGATTGAGATTATAGATGAGTTCCCGACCTTTG	1920
Qy	1921	TCAGTTCTAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACACTGACCTAGAAGTAG	1980
Db	1921	TCAGTTCTAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACACTGACCTAGAAGTAG	1980
Qy	1981	CCCACAAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTCAATTGGCTTGTGTCAGGAT	2040
Db	1981	CCCACAAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTCAATTGGCTTGTGTCAGGAT	2040
Qy	2041	TGCCCCATGACCTTTCTTTCAAGAGTATACAACCTAAAGAGGAAGTTCATGTCCCAGATG	2100
Db	2041	TGCCCCATGACCTTTCTTTCAAGAGTATACAACCTAAAGAGGAAGTTCATGTCCCAGATG	2100
Qy	2101	AGTTCTCCAAAGATAGGGGTGATGTTTCAAAGGTGCCGTA CTGCCTCCAGATGTTTCTG	2160
Db	2101	AGTTCTCCAAAGATAGGGGTGATGTTTCAAAGGTGCCGTA CTGCCTCCAGATGTTTCTG	2160
Qy	2161	CTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAAACCCAAAGTTCTTGTGAAAGAAG	2220
Db	2161	CTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAAACCCAAAGTTCTTGTGAAAGAAG	2220
Qy	2221	CCGAGAGAAAACTTCCTTCTGATACAGAAAAAGAGCGAAGATCTCCATCTGCTATATTTT	2280
Db	2221	CCGAGAGAAAACTTCCTTCTGATACAGAAAAAGAGCGAAGATCTCCATCTGCTATATTTT	2280
Qy	2281	CAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAGA	2340
Db	2281	CAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAGA	2340
Qy	2341	CTGGAGTGGTGTTTGGTGCCAGCTTGTTCTGCTGCTCTCGCTGACAGTATTCAGCATTG	2400

Db	2341	 CTGGAGTGGTGTGTTGGTGCCAGCTGTTCTCTGCTGCTCTCGCTGACAGTATTCAGCATTG	2400
Qy	2401	 TGAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATAT	2460
Db	2401	 TGAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATAT	2460
Qy	2461	 ATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATTTCAGGGCATATT	2520
Db	2461	 ATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATTTCAGGGCATATT	2520
Qy	2521	 TGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTTCAGAAGTACAGCAATTCTGCTCTTG	2580
Db	2521	 TGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTTCAGAAGTACAGCAATTCTGCTCTTG	2580
G	Qy	2581	CTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGTTGATGAGTATAGTAG 2640
Db	2581	 GTCATGTAACTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGTTGATGATTTAGTTG	2640
Qy	2641	 ATTCTCTGAAGTTTGCAGTGTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTCAATG	2700
Db	2641	 ATTCTCTGAAGTTTGCAGTGTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTCAATG	2700
Qy	2701	 GTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCCTGTTATTTATGAAC	2760
Db	2701	 GTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCCTGTTATTTATGAAC	2760
Qy	2761	 GGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTTAAAGATGCTA	2820
Db	2761	 GGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTTAA1CCTGCTA	2820
Qy	2821	 TGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGAGAAAGCCTGA	2880
Db	2821	 TGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGAGAAAGCCTGA	2880
Qy	2881	 AAGAGTTAACAATAGAGGAGTTTATCTTTAAAGGGGATATTCATTTGATTCCATTGGGGA	2940
Db	2881	 AAGAGTTAACAATAGAGGAGTTTATCTTTAAAGGGGATATTCATTTGATTCCATTGGGGA	2940
Qy	2941	 GGGTCAGGGAAGAACAAGCCTTGACATTGCAGTGCAGTTTCACAGATCTTTATTTTATAG	3000
Db	2941	 GGGTCAGGGAAGAACAAGCCTTGACATTGCAGTGCAGTTTCACAGATCTTTATTTTATAG	3000
Qy	3001	 CAACGCAGTGTCTGAGGAAAAATGACCTGTCTTGACTGCCCTGTGTTTCATCATCTTAAGT	3060
Db	3001	 CAACGCAGTGTCTGAGGAAAAATGACCTGTCTTGACTGCCCTGTGTTTCATCATCTTAAGT	3060
Qy	3061	 ATTGTAAGCTGCTATGTATGGATTTAAATCGTAATCATATTTGTTTTCTGTATGAGGC	3120
Db	3061	 ATTGTAAGCTGCTATGTATGGATTTAAATCGTAATCATATTTGTTTTCTGTATGAGGC	3120
Qy	3121	 ACTGGTGAATAAACAAAGATCTGAGAAAGCTGTATATTACACTTTGTGCGAGGTAGTCTT	3180
Db	3121	 ACTGGTGAATAAACAAAGATCTGAGAAAGCTGTATATTACACTTTGTGCGAGGTAGTCTT	3180
Qy	3181	 GCTGTATTTGGGGAATTGCAAAGAAAGTGGAGCTGACAGAAATAACCCCTTTTCACAGTTT	3240

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Db      3181 GCTGTATTTTGGGGAATTGCAAAGAAAGTGGAGCTGACAGAAATAACCCTTTTCACAGTTT 3240
Qy      3241 GTGCACTGTGTACGGTCTGTGTAGGTTGATGCAGATTTTCTGAAATGAAATGTTTAGACG 3300
        |||
Db      3241 GTGCACTGTGTACGGTCTGTGTAGGTTGATGCAGATTTTCTGAAATGAAATGTTTAGACG 3300
Qy      3301 AGATCATGCCACCAAGGCAGGAGTGAAAAAGCTTGCCTTTCCTGGTATGTTCTAGGTGTA 3360
        |||
Db      3301 AGATCATGCCACCAAGGCAGGAGTGAAAAAGCTTGCCTTTCCTGGTATGTTCTAGGTGTA 3360
Qy      3361 TTGTGAAATTTACTGTTGTATTAATTGCCAATATAAGTAAATATAGATTATATATATCTA 3420
        |||
Db      3361 TTGTGAAATTTACTGTTGTATTAATTGCCAATATAAGTAAATATAGATTATATATATCTA 3420
Qy      3421 TATATAGTGTTCACGAAGCTTAGCCCTTTACCTTCCCAGCTGCCCCACAGTGCTTGATA 3480
        |||
Db      3421 TATATAGTGTTCACGAAGCTTAGCCCTTTACCTTCCCAGCTGCCCCACAGTGCTTGATA 3480
Qy      3481 CTTCTGTTCATGGGTTTTATGTGTGTAGTCCCAAAGCACATAAGCTAGGGAGAAACGTACT 3540
        |||
Db      3481 CTTCTGTTCATGGGTTTTATGTGTGTAGTCCCAAAGCACATAAGCTAGGGAGAAACGTACT 3540
Qy      3541 TCTAGGCGCACTACCATCTGTTTTCAACACGAACCGACGCCATGCAAACAGAACTCCTCA 3600
        |||
Db      3541 TCTAGGCGCACTACCATCTGTTTTCAACACGAACCGACGCCATGCAAACAGAACTCCTCA 3600
Qy      3601 ACATAAACTTCACTGCACAGACTTACTGTAGTTAATTTTATCACAAACTCTGGACTGAAT 3660
        |||
Db      3601 ACATAAACTTCACTGCACAGACTTACTGTAGTTAATTTTATCACAAACTCTGGACTGAAT 3660
Qy      3661 CTAADATCTCTCAAAATGTTTGCAAATATCAAACATTGTTATGTA1050X10 AATGA 3720
        |||
Db      3661 CTAATGCTTCCAAAAATGTTTGCAAATATCAAACATTGTTATGTAAGAAAAATATAAATGA 3720
Qy      3721 CGATTTATACAATTGTGGTTTAAGCTGTATTGAACTAAATCTGTGGAATGCATTGTGAAC 3780
        |||
Db      3721 CGATTTATACAATTGTGGTTTAAGCTGTATTGAACTAAATCTGTGGAATGCATTGTGAAC 3780
Qy      3781 TGTAAGCAAGATATCAATAAGCTTATAGACTTAAAAAAAAAAAAAAAAAAAA 3833
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Db      3781 TGTAAGCAAGATATCAATAAGCTTATAGACTTAAAAAAAAAAAAAAAAAAAA 3833

```

RESULT 2

ABS70449

ID ABS70449 standard; cDNA; 4822 BP.

XX

AC ABS70449;

XX

DT 27-NOV-2002 (first entry)

XX

DE Human bone remodelling gene #106.

XX

KW Bone remodelling; osteoporosis; human; gene; ss.

XX

OS Homo sapiens.

XX

PN US6426186-B1.
 XX
 PD 30-JUL-2002.
 XX
 PF 18-JAN-2000; 2000US-0484970.
 XX
 PR 18-JAN-2000; 2000US-0484970.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 XX
 PI Jones KA, Volkmuth W, Walker MG;
 XX
 DR WPI; 2002-673014/72.
 XX
 PT A combination of polynucleotides which are co-expressed with genes
 PT known to be involved in bone remodeling and osteoporosis are useful in
 PT an array for the diagnosis of bone remodeling and osteoporosis
 PT associated disorders -
 XX
 PS Claim 1; Column 283-288; 206pp; English.
 XX
 CC The invention relates to a combination comprising a number of
 CC substantially purified and isolated polynucleotides which are
 CC co-expressed with genes known to be involved in bone remodelling and
 CC osteoporosis. The invention is used to diagnose disorders associated
 CC with bone remodelling o orosis. ABS70344-ABS70512 represent |
 CC human bone remodelling genes of the invention.
 XX
 SQ Sequence 4822 BP; 1441 A; 1046 C; 1073 G; 1247 T; 15 other;

Query Match 70.1%; Score 2687.8; DB 24; Length 4822;
 Best Local Similarity 85.6%; Pred. No. 0;
 Matches 3333; Conservative 0; Mismatches 458; Indels 104; Gaps 27;

Qy	1	CTATCTCCTCTCTCAGCCGCTGCTTTTAAAGAACGTGAATACCTTGGTGATTTACCAGCA	60
Db	964	CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAATTTGTCAACA	1023
Qy	61	GTACTGCCCACTGAAGGAACACTTCCAGCAACTTCAAATGAAGCTTCTAAAGCATTCTCA	120
Db	1024	GTATTACCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA	1083
Qy	121	GAGAAGGCAAAAAATCCATTTGTAGAGAGAAATTTAACAGAATTTTCAGAATTGGAATAT	180
Db	1084	GAGAAGGCAAAAACTCTACTCATAGATAGAGATTTAACAGAGTTTTCAGAATTAGAATAC	1143
Qy	181	TCAGAAATGGAATCATCATTAGTGGCTCTCAAAGGCAGAACCTGCCGTAACAGTAGCG	240
Db	1144	TCAGAAATGGGATCATCGTTAGTGTCTCTCCAAAGCAGAATCTGCCGTAATAGTAGCA	1203
		5	
Qy	241	AATCCTAGGGACGAAATAGTTGTGAGGAGTAGAGATAAAGAAGAGGACTTAGTTAGTCTT	300
Db	1204	AATCCTAGGGAAGAAATAATCGTGAAAAATAAGATGAAGAAGAGAACTTAGTTAGTAAT	1263
Qy	301	AACATCCTTCATACTCAGCAGGAGTTATCTACAGTCCTTACGAAATCAGTTGAAGAAGAA	360
Db	1264	AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT	1323

Qy		361	GATAGAGTTCTGTCTGCCGAAAAAACAAGGCACAGTTTTAAGGAAAAGGGAGTGTCAGCA	420
Db		1324	GA---AGTTGTGTCTTCAGAAAAAGCAAAGACAGTTTTTAATGAAAAGAGAGTTGCAGTG	1380
Qy		421	GAAGCCTTCTATGGGGGAGGAATATGCAGACTTCAAACCATTGTGAGCGAGTATGGGAAGTG	480
Db		1381	GAAGCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTGTGAGCGAGTATGGGAAGTG	1440
Qy		481	AAAGATACTTACAAGCAAGATAGTGATGTTTTGATTGCTGGAGGTAATATAGAGAGCAAA	540
Db		1441	AAAGATAGT---AAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAAATCGAGAGCAAC	1497
Qy		541	TTGGAAGGTAAAGTGGATAAGAAACACTTTTCAGATAGCCCTTGAACAAACAAATCGTGAA	600
Db		1458	TTGGAAGGTAAAGTGGATAAAAAATGTTTTGCAGATAGCCCTTGAACAAACTAATCACGAA	1557
Qy		601	AAAGATAGTGAAAGCAGTAATGATGACACTTCATTTCCCAGTACACCAGAAGCTGTAAGA	660
Db		1558	AAAGATAGTGAGAGTAGTAATGATGATACTTCCTTTCCCCAGTACGCCAGAAGGTATAAAG	1617
Qy		661	GGTGGTTCCGGAGCGTACATCACGTGTGCTCCCTTTAACCC--CAACAACTGAGAATGTT	717
Db		1618	GATCGTTCCAGGAGCATATATCACATGTGCTCCCTTTAACCCAGCAGCAACTGAGAGCATT	1677
Qy		718	TCAACAAACATTTTTCCTTGTGGAAGATCATACTTCGGAAAATAAGACAGATGAAAAA	777
Db		1678	GCAACAAACATTTTTCCTTTGTAGGAGATCCTACTTCAGAAAATAAGACCGATGAAAAA	1737
Qy		778	AAGA--TAGAAAAAAAAAGGCACAAATTGTAAACAGAGAAGAATGCAAGTGTCAAGACATC	835
Db		1738	AAAAATAGAAGAAAAGAAGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAAACATC	1797
Qy		836	AAACCC-TTTCCTTATGGCAGCACAGGAGTCTAAGACAGATTACGTTACAACAGATCATG	894
Db		1798	AAACCCTTTACTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATT	1857
Qy		895	TGTCAAAGGTGACCGAGGAAGTAGTGGCAAACATGCCTGAAGGTCTAACCCAGATTTGG	954
Db		1858	TAACAAAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAG	1917
Qy		955	TTCAGGAAGCATGTGAAAGTGAATTGAATGAAGCTACTGGTACAAAAATTGCCTTTGAAA	1014
Db		1918	TACAGGAAGCATGTGAAAGTGAATTGAATGAAGTACTGGTACAAAGATTGCTTATGAAA	1977
Qy		1015	CAAAAATGGACCTGGTTCAAACCTCAGAAGCTGTGCAGGAGTCACTTTACCCTGTAAACAC	1074
Db		1978	CAAAAATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCAC	2037
Qy		1075	AGCTTTGCCCATCTTTTGAAGAATCTGAAGCTACTCCGTACCCGGTTTTGCCTGACATTG	1134
Db		2038	AGCTTTGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTACCAGTTTTGCCTGACATTG	2097
Qy		1135	TCATGGAAGCACCATTA AAATTCTGTAGTTCCTAGTGCTGGTGCTTCTGCAGTGCAGCTCA	1194
Db		2098	TTATGGAAGCACCATTTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCA	2157

Qy	1195	GTTCATCACCATTAGAAAACCTCTCCCTTCAGTTAATTATGAAAGCATAAAAGTTTGAGCCTG	1254
Db	2158	GCTCATCACCATTAGAAAGC---TTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTG	2214
Qy	1255	AAAATCCCCCACCATATGAGGAGGCCATGAATGTATCACTAAAAAAGAATCAGGAATGA	1314
Db	2215	AAAACCCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAA	2274
Qy	1315	ATGAAGAAATCACAGAGCCTGAAGGTATTAGTGTAGCTGTTTCAGGAAACAGAAGCTCCTT	1374
Db	2275	AGGAAGAAATTAAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTT	2334
Qy	1375	ATATATCTATTGCATGTGATTTAATTAAAGAAACAAAGATCTCTACTGAACCGACTCCAG	1434
Db	2335	Homo sapieTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCAGCTCCGG	2394
Qy	1435	ATTTCTCTAGTTATTTCAGAAATAGCAGAAGTTGCACAGCCAGTGCCCGAGCATTCTGAGC	1494
Db	2395	ATTTCTCTGATTATTTCAGAAATGGCAAAAGTTGAACAGCCAGTGCTTGATCATTCTGAGC	2454
Qy	1495	TAGTTGAAGATTCTCTCCCCGATTCTGAACCAAGTTGACTTATTTAGTGTATGATTCAATAC	1554
Db	2455	TAGTTGAAGATTCTCTCACCTGATTCTGAACCAAGTTGACTTATTTAGTGTATGATTCAATAC	2514
Qy	1555	CCGAAGTTCCACAAAAACAAGATGAAGCTGTAATACTTGTGAAAGAAAACCTCACTGAAA	1614
Db	2515	CTGACGTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGA	2574
Qy	1615	TTTCATCTGAGTCAATGACAGGACATGACAATAAGGGAAAACTCAGTGCCTTACCATCAC	1674
Db	2575	CTTCATTTGAGTCAATGATAGAATATGAAAATAAGGAAAACTCAGTGCCTTTGC---CAC	2631
Qy	1675	CTGAGGGAGGAAAACCGTATTTGGAGTCTTTTCAGCCAGTTTAGGCATCACAAAAGATA	1734
Db	2632	CTGAGGGAGGAAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATA	2691
Qy	1735	CCTTAGCACCTGATGAAGTTTCAGCATTGACCCAAAAGGAGAAA TCCCTTTGCAGATGG	1794
Db	2692	CCCTGTTACCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAATTCCCTTTGCAGATGG	2751
Qy	1795	AGGAGCTCAATACTGCAGTTTATTCAAGTGATGGCTTATTCATTGCTCAGGAAGCAAACC	1854
Db	2752	AGGAGCTCAGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGA	2811
Qy	1855	TAAGAGAAAGTGAAACATTTTCAGATTTCATCTCCGATTGAGATTATAGATGAGTTCCCGA	1914
Db	2812	TAAGAGAAACTGAAACGTTTTCAGATTTCATCTCCAATTGAAATTATAGATGAGTTCCCTA	2871
Qy	1915	CCTTTGTTCAGTTCTAAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACACTGACCTAG	1974
Db	2872	CATTGATCAGTTCTAAAAGTATTCTTCTAAAATTAGCCAGGGAATATACTGACCTAG	2931
Qy	1975	AAGTAGCCACAAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTTCATTGGCTTGTG	2034
Db	2932	AAGTATCCACAAAAGTGAAATTGCTAATGCCCCGATGGAGCTGGGTTCATTGCCTTGCA	2991
Qy	2035	CAGGATTGCCCATGACCTTTCTTTCAAGAGTATACAACC-----TAAAGAGGAAGTTC	2088

Db 3832 TGAAAACGCCCAAAATAATTA-----GTAGGAGTTCATCTTTAAAGGGGATATTCATTTG 3886

Qy 2928 ATTCCATTGGGGAGGGTCAGGGAAGAACAAAGCCTTGACATTGCAGTGCAGTTTCAC--- 2984
 ||| | |||||||||||||||||||| | | |||||| ||||||||||||||||||||

Db 3887 ATTATACGGGGGAGGGTCAGGGAAGAACGAA-CCTTGACGTTGCAGTGCAGTTTCACAGA 3945

Qy 2985 -----AGATCTTTATTTTTTAGCAACGCAGTG-TCTGAGGAAAAATGACCTGTCTTGA 3035
 |||||||||||||||||||| | | | | ||||||||||||||||||||

Db 3946 TCGTTGTTAGATCTTTATTTTTTAGCCATGCACTGTTGTGAGGAAAAATTACCTGTCTTGA 4005

Qy 3036 CTGCCCTGTGTTTCATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTTAAATCGTAAT 3095
 |||| | |||||||||||||||||||||||||||||||||||||||||||| | |||||

Db 4006 CTGCCATGTGTTTCATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTTAAACCGTAAT 4065

Qy 3096 CATATTTGTTTTCTGTATGAGGCACCTGGTGAATAAACAAAGATCTGAGAAAGCTGTAT 3155
 |||| | |||||||| | |||||||||||||| | | || | |||||

Db 4066 CATA--TCTTTTCTATCTGAGGCACCTGGTGA-----ATAAAAAACCTGTAT 4112

Qy 3156 ATTACACTTTGTGCGAGGTAGTCTTGCTGTAT-TTGGGGAATTGCAAAGAAAGTGAGCT 3214
 ||| |||||| | || | |||||| | | || | |||| | || | |||||

Db 4113 ATTTTACTTTGTGTCAGATAGTCTTGCCGCATCTTGGCAAGTTCAGAGATGGTGGAGCT 4172

Qy 3215 -----GACAGAAATAACCCTTTTTCAGTTTGTGCACTGTGTACGGTCTGTGTAGGT 3266
 | | || | | | | || | || | |||||| |||||| |||||| ||

Db 4173 AGAAAAAAAAAAAAAAAAAAGCCCTTTTCAGTTTGTGCACTGTGTATGGTCCGTGTAGAT 4232

Qy 3267 TGATGCAGATTTTCTGAAATGAAA----TGTTTAGACGAGATCATGCCACCAAGGCAGGA 3322
 |||||||||||||||||| || |||||||||||||| || | || |||||

Db 4233 TGATGCAGATTTTCTGAAATGAAATGTTTGTGTTAGACGAGATCATACCGGTAAAGCAGGA 4292

Qy 3323 GTGAAAAGCTTGCCTTTCTGGTATGTTCTAGGTGTATTGTGAAATTTACTGTTGTATT 3382
 ||| |||||| | || | |||||||||||||||||||||| || ||||| |||||

Db 4293 ATGACAAAGCTTG-CTTTCTGGTATGTTCTAGGTGTATTGTGACTTTTACTGTTATATT 4351

Qy 3383 AATTGCCAATATAAGTAAATATAGATTATATATATCTATATATAGTGTTTCACGAAGCTT 3442
 |||||||||||||||||| || |||||||||| |||||| |||||| |||||

Db 4352 AATTGCCAATATAAGTAAATATAGATTATATATG-----TATAGTGTTTCACAAAGCTT 4405

Qy 3443 AGCCCTTTTACCTTCCAGCTGCCCCACAGTGCTTGATACT-----TCTGTCATGGGTTT 3496
 || |||||| | || | |||||| |||||| || | || |||| | ||

Db 4406 AGACCTTTTACCTT-CCAGCCACCCACAGTGCTTGATATTTTACAGTGCAGTTCATTGGTTA 4464

Qy 3497 TATGTGTGTAGTCCCAAAGCACATAAGCTAGGGAGAAACGTACTTCTAGGCGCACTACCA 3556
 || |||||| | |||||||||||||| || | || |||||| |||||| ||

Db 4465 TACATGTGTAGTTCCCAAAGCACATAAGCTAGAAGAAGAAATATTTCTAGGAGCACTACCA 4524

Qy 3557 TCTGTTTTCAACACGAACCGACGCCATGCAACAGAACTCC-TCAACATAAACTTCACTG 3615
 |||||| |||| | || | || | |||||| || || | || || ||

Db 4525 TCTGTTTTCAACATGAA---ATGCCACACATAGAATCCAACAACATCAATTTTCATTG 4581

Qy 3616 CACAGACTTACTGTAGTTAATTTTATCAC--AAACTCTGGACTGAATCTAATGCTTCCAA 3673
 |||||| |||||| |||| | || | || || |||||| |||||| |||||

Db 4582 CACAGACTGACTGTAGTTAATTTTGTACAGAATCTATGGACTGAATCTAATGCTTCCAA 4641

Qy 3674 AAA-----TGTTTGCAAATATCAAACATTGTTATGTAAGAAAATAT-----AAAT 3718
 ||| || | |||||| |||||| || || || || || || || || ||

Db 4642 AAATGTTGTTTGTGTTTGCAAATATCAAACATTGTTATGCAAGAAATTATTAATTACAAAAT 4701

Qy 3719 GACGATTTTATACAATTGTGGTTTTAAGCTGTATTGAACATAAATCTGTGGAATGCATTGTGA 3778
|| ||||||| | ||||||||||||||| | |||||||||||||||
Db 4702 GAAGATTTTATACCATTGTGGTTTTAAGCTGTACTGAACATAAATCTGTGGAATGCATTGTGA 4761

Qy 3779 ACTGTAAAAGCAAAGTATCAATAAAGCTTATAGACTTAAAAAAAAAAAAAAAAAAAA 3833
||| ||||||||||||||| | |||
Db 4762 ACTGTAAAAGCAAAGTATCAATAAAGCTTATAGACTTAAANGNNANNAGNGAAA 4816

RESULT 3

ABV94680

ID ABV94680 standard; cDNA; 4632 BP.

XX

AC ABV94680:

XX

DT 14-JAN-2003 (first entry)

XX

DE Human pancreatic cancer expressed cDNA SEQ ID NO 53.

XX

KW Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;

KW cytostatic; tumour; gene; ss.

XX

OS Homo sapiens.

XX

PN WO200260317-A2.

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PD 08-AUG-2002.

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PF 30-JAN-2002; 2002WO-US02A

XX

PR 30-JAN-2001; 2001US-265305P.

PR 31-JAN-2001; 2001US-265682P.

PR 09-FEB-2001; 2001US-267568P.

PR 21-MAR-2001; 2001US-278651P.

PR 28-APR-2001; 2001US-287112P.

PR 16-MAY-2001; 2001US-291631P.

PR 12-JUL-2001; 2001US-305484P.

PR 20-AUG-2001; 2001US-313999P.

PR 27-NOV-2001; 2001US-333626P.

XX

PA (CORI-) CORIXA CORP.

XX

PI Benson DR, Kalos MD, Lodes MJ, Persing DH, Hepler WT, Jiang Y;

XX

DR WPI; 2002-627435/67.

DR P-PSDB; ABP68600.

XX

PT New isolated polynucleotide and pancreatic tumor polypeptides, useful

PT for diagnosing, preventing and/or treating cancer, particularly

PT pancreatic cancer -

XX

PS Claim 1; SEQ ID NO 53; 300pp + Sequence Listing; English.

XX

CC The invention relates to an isolated polynucleotide (I) comprising: (a)

CC any of a group of over 4000 nucleotide sequences (ABV94628-ABV99445);

CC (b) complements of (a); (c) sequences consisting of at least 20

CC contiguous residues of (a); (d) sequences that hybridize to (a), under
 CC moderately stringent conditions; (e) sequences having at least 75% or 90%
 CC identity to (a); or (f) degenerate variants of (a). Polypeptides
 CC (ABP68596-ABP68637) encoded by (I) and oligonucleotide can be used to
 CC detect cancer in a patient and compositions comprising polypeptides,
 CC polynucleotides, antibodies, fusion proteins, T cell populations and
 CC antigen presenting cells expressing the polypeptide are useful in
 CC treating pancreatic cancer and stimulating an immune response. The
 CC polynucleotides can be used as probes or primers for nucleic acid
 CC hybridisation, in the design and preparation of ribozyme molecules for
 CC inhibiting expression of the tumour polypeptides and proteins in the
 CC tumour cells, in vaccines and for gene therapy.
 CC Note: The sXs data for this patent did not form part of the printed0;
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 4632 BP; 1398 A; 1013 C; 1011 G; 1210 T; 0 other;

Query Match 69.1%; Score 2649.8; DB 24; Length 4632;
 Best Local Similarity 85.0%; Pred. No. 0;
 Matches 3292; Conservative 0; Mismatches 442; Indels 137; Gaps 24;

Qy	1	CTATCTCCTCTCTCAGCCGCTGCTTTTAAAGAACGTGAATACCTTGGTGATTTACCAGCA	60
Db	853	CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAATTTGTCAACA	912
Qy	61	GTAAGGCAAGGAACACTTCCAGCAACTTCAAATGAAGCTTCTAAAGCATTCTCA	120
Db	913	GTATTACCCACTGAAGGAACACTTCAAGAAAATGTCAAGCTTCTAAAGAGGTCTCA	972
Qy	121	GAGAAGGCAAAAAATCCATTTGTAGAGAGAAATTTAACAGAAATTTTCAGAATTGGAATAT	180
Db	973	GAGAAGGCAAAAACTCTACTCATAGATAGAGATTTAACAGAGTTTTCAGAATTAGAATAC	1032
Qy	181	TCAGAAATGGAATCATCATTCAAGGCTCTCAAAGGCAGAACCTGCCGTAACAGTAGCG	240
Db	1033	TCAGAAATGGGATCATCGTTCAAGTGTCTCTCCAAAAGCAGAAATCTGCCGTAATAGTAGCA	1092
Qy	241	AATCCTAGGGACGAAATAGTTGTGAGGAGTAGAGATAAAGAAGAGGACTTAGTTAGTCTT	300
Db	1093	AATCCTAGGGAAGAAATAATCGTGAAAAATAAGATGAAGAAGAGAAGTTAGTTAGTAAT	1152
Qy	301	AACATCCTTCATACTCAGCAGGAGTTATCTACAGTCCTTACGAAATCAGTTGAAGAAGAA	360
Db	1153	AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT	1212
Qy	361	GATAGAGTTCTGTCTCCAGAAAAACAAAGGACAGTTTAAAGGAAAAGGGAGTTGCAGCA	420
Db	1213	GA---AGTTGTGTCTTCAGAAAAAGCAAAGACAGTTTAAATGAAAAGAGAGTTGCAGTG	1269
Qy	421	GAAGCTTCTATGGGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG	480
Db	1270	GAAGCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG	1329
Qy	481	AAAGATACTTACAAGCAAGATAGTGATGTTTTGATTGCTGGAGGTAATATAGAGAGCAAA	540
Db	1330	AAAGATAGT---AAGGAAGATAGTGATGTTGGCTGCTGGAGGTAAAATCGAGAGCAAC	1386

Qy	541	TTGGAAGGTAAAGTGGATAAGAAACACTTTTCAGATAGCCTTGAACAAACAAATCGTGAA	600
Db	1387	TTGGAAGGTAAAGTGGATAAAAAATGTTTTCAGATAGCCTTGAACAAACTAATCACGAA	1446
Qy	601	AAAGATAGTGAAAGCAGTAATGATGACACTTCATTTCCAGTACACCAGAAGCTGTAAGA	660
Db	1447	AAAGATAGTGAGAGTAGTAATGATGATACTTCTTTCCCAAGTACGCCAGAAGGTATAAAG	1506
Qy	661	GGTGGTTCCGGAGCGTACATCACGTGTGCTCCCTTTAACC---CAACAACAGAGAATGTT	717
Db	1507	GATCGTTCAGGAGCATATATCACATGTGCTCCCTTTAACCAGCAGCAACTGAGAGCATT	1566
Qy	718	TCAACAAACATTTTTCCCTTGTTGGAAGATCATACTTCGGAAAAATAAGACAGATGAAAAA	777
Db	1567	GCAACAAACATTTTTCTTTGTTAGGAGATCCTACTTCAGAAAAATAAGACCGATGAAAAA	1626
Qy	778	AAGATAGAA-AAAAAAGGCACAAATTGTAACAGAGAAGAATGCAAGTGTCAAGACATCA	836
Db	1627	AAAATAGAAGAAAAGAAGGCCAAATAGTAACAGAGAAGAATACTAGCACCAAAACATCA	1686
Qy	837	AACCCTTTCTTATGGCAGCACAGGAGTCTAAGACAGATTACGTTCAACAGATCATGTG	896
Db	1687	AACCCTTTCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCAACAGATAATTTA	1746
Qy	897	TCAAAGGTGACCGAGGAAGTAGTGGCAAACATGCCTGAAGGTCTAACCCAGATTTGGTT	956
Db	1747	ACAAAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTA	1806
Qy	957	CAGGAAGCATGTGAAAGTGAATTGAATGAAGCTACTGGTACAAAAATTGCCTTTGAAACA	1016
Db	1807	CAGGAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACA	1866
Qy	1017	AAAATGGACCTGGTTCAAACCTTCAGAAGCTGTGCAGGAGTCACTTTACCTGTAAACACAG	1076
Db	1867	AAAATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAG	1926
Qy	1077	CTTGCCCATCTTTTGAAGAATCTGAAGCTACTCCGTCACCGGTTTTGCCTGACATTGTC	1136
Db	1927	CTTGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGCCTGACATTGTT	1986
Qy	1137	ATGGAAGCACCATTAAATTCTGTAGTTCCTAGTGCTGGTGCTTCTGCAGTGCAGCTCAGT	1196
Db	1987	ATGGAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCAGC	2046
Qy	1197	TCATCACCATTAGAACTCTTCCTTCAGTTAATTATGAAAGCATAAAAGTTTGAGCCTGAA	1256
Db	2047	TCATCACCATTAGAAGC---TTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAA	2103
Qy	1257	AATCCCCCACCATATGAGGAGGCCATGAATGTATCACTAAAAAAGAATCAGGAATGAAT	1316
Db	2104	AATCCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAG	2163
Qy	1317	GAAGAAATCACAGAGCCTGAAGGTATTAGTGTAGCTGTTGAGGAAACAGAAGCTCCTTAT	1376
Db	2164	GAAGAAATTAAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTAT	2223

Qy	1377	ATATCTATTGCGATGTGATTTTAATTAAAGAAAACAAAGATCTCTACTGAACCCGACTCCAGAT	1436
Db	2224		
Qy	1437	TTCTCTAGTTATTTCAGAAATAGCAGAAGTTGCACAGCCAGTGCCCGAGCATTCTGAGCTA	1496
Db	2284		
Qy	1497	GTTGAAGATTCCCTCCCCGATTCTGAACCAGTTGACTTATTTAGTGTATGATTCAATACCC	1556
Db	2344		
Qy	1557	GAAGTTCCACAAAAACAAGATGAAGCTGTAATACTTGTGAAAGAAAACCTCACTGAAATT	1616
Db	2404		
Qy	1617	TCATCTGAGTCAATGACAGGACATGACAATAAGGGAAAACTCAGTGCCTCACCATCACCT	1676
Db	2464		
Qy	1677	GAGGGAGGAAAACCGTATTTGGAGTCTTTTCAGCCAGTTTAGGCATCACAAAAGATACC	1736
Db	2521		
Qy	1737	TTAGCACCTGATGAAGTTTCAGCATTGACCCAAAAGGAGAAAATCCCTTTGCAGATGGAG	1796
Db	2581		
Qy	1797	GAGCTCAATACTGCAGTTTATTCAAGTGATGGCTTATTCAATTGCTCAGGAAGCAAACCTA	1856
Db	2641		
Qy	1857	AGAGAAAGTGAAACATTTTCAGATTTCATCTCCGATTGAGATTATAGATGAGTTCCCGACC	1916
Db	2701		
Qy	1917	TTTGTGAGTTCTAAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACACTGACCTAGAA	1976
Db	2761		
Qy	1977	GTAGCCACAAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTCAATTGGCTTGTGCA	2036
Db	2821		
Qy	2037	GGATTGCCCCATGACCTTTCTTTCAAGAGTATACAACC-----TAAAGAGGAAGTTCAT	2090
Db	2881		
Qy	2091	GTCCCGAGATGAGTTCTCCAAAGATAGGGGTGATGTTTCAAAGGTGCCCGTACTGCCTCCA	2150
Db	2941		
Qy	2151	GATGTTTCTGCTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAAACCCAAAGTTCTT	2210
Db	3001		
Qy	2211	GTGAAAGAAGCCGAGAGAAAACTTCCTTCTGATACAGAAAAAGAGCGAAGATCTCCATCT	2270

Db	3061		GTGAAAGAAGCTGAGAAAAA	CTTCCTTCCGATACAGAAAAA	AGGACAGATCACCATCT	3120
Qy	2271		GCTATATTTTCAGCAGAGCTGAGTAA	AACCTTCAGTTGTTGACCTCCTCT	ACTGGAGAGAC	2330
Db	3121		GCTATATTTTCAGCAGAGCTGAGTAA	AACCTTCAGTTGTTGACCTCCTGT	ACTGGAGAGAC	3180
Qy	2331		ATTAAGAAGACTGGAGTGGTGT	TTGGTGCCAGCTTGTTCCCTGCTGCTCT	CGCTGACAGTA	2390
Db	3181		ATTAAGAAGACTGGAGTGGTGT	TTGGTGCCAGCCTATTCCCTGCTGCTTT	CATTGACAGTA	3240
Qy	2391		TTCAGCATTGTGAGTGTAACGGCCT	TACATTGCCCTTGCCCTGCTCTCTGT	GACTATCAGC	2450
Db	3241		TTCAGCATTGTGAGCGTAACAGCCT	TACATTGCCCTTGCCCTGCTCTCTGT	GACCATCAGC	3300
Qy	2451		TTTAGGATATATAAGGGTGTGATCC	AGGCTATCCAGAAATCTGATGAAGGCC	ACCCATTC	2510
Db	3301		TTTAGGATATACAAGGGTGTGATCC	AAGCTATCCAGAAATCAGATGAAGGCC	ACCCATTC	3360
Qy	2511		AGGGCATATTTGGAATCTGAAGTTG	CTATATCTGAGGAGTTGGTTCAGAAGT	ACAGCAAT	2570
Db	3361		AGGGCATATCTGGAATCTGAAGTTG	CTATATCTGAGGAGTTGGTTCAGAAGT	ACAGTAAT	3420
Qy	2571		TCTGCTCTTGGTCATGT	TAACTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGTTGAT	2630	
Db	3421		TCTGCTCTTGGTCATGTGAACTGC	CAGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGAT	3480	
Qy	2631		GATTTAGTTGATTCTCTGAAGTTT	GCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCC	2690	
Db	3481		GATTTAGTTGATTCTCTGAAGTTT	GCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCC	3540	
Qy	2691		TTGTTCAATGGTCTGACACTACTA	ATTTTGGCTCTGATTTCACTCTTCAGTGTTCCCTGTT	2750	
Db	3541		TTGTTTAAATGGTCTGACACTACT	GATTTTGGCTCTCATTTCACTCTTCAGTGTTCCCTGTT	3600	
Qy	2751		ATTTATGAACGGCATCAGGCGCAA	ATAGATCATTATCTGGGACTTGCAAATAAGAATGTT	2810	
Db	3601		ATTTATGAACGGCATCAGGCACAG	ATAGATCATTATCTAGGACTTGCAAATAAGAATGTT	3660	
Qy	2811		AAAGATGCTATGGCTAAAATCCA	AGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGA	2870	
Db	3661		AAAGATGCTATGGCTAAAATCCA	AGCAAAAATCCCTGGATTGAAGCGCAAAGCTGAATGA	3720	
Qy	2871		GAAAGCCTGAAAGAGTTAA	CAATAGAGGAGTTTATCTTTAAAGGGGATATTCATTTGATT	2930	
Db	3721		AAACGCCCAAATAATTAGT----	AGGAGTTCATCTTTAAAGGGGATATTCATTTGATT	3775	
Qy	2931		CCATTGGGGAGGGTCAGGGA	AGAACAAAGCCTTGACATTGCAGTGCAGTTTCACAGATCT	2990	
Db	3776	AT-----			ACGGATCT	3785
Qy	2991		TTATTTT	TAGCAACGCAGTG-TCTGAGGAAAAATGACCTGTCTTGACTGCCCTGTGTTCA	3049	
Db	3786		TTATTTT	TAGCCATGCACTGTTGTGAGGAAAAATTACCTGTCTTGACTGCCATGTGTTCA	3845	
Qy	3050		TCATCTTAAGTATTGTAAGCTGCT	TATGTATGGATTAAATCGTAATCATATTTGTTTTTC	3109	

Db	3846	TCATCTTAAGTATTGTAAGCTGCTATGTATGGATTTAAACCGTAATCATA--TCTTTTTC	3903
Qy	3110	CTGTATGAGGCACTGGTGAATAAAACAAAGATCTGAGAAAGCTGTATATTACACTTTGTCTG	3169
Db	3904	CTATCTGAGGCACTGGTGGA-----ATAAAAACCTGTATATTTTACTTTGTGTG	3952
Qy	3170	CAGGTAGTCTTGCTGTAT-TTGGGGAATTGCAAAGAAAGTGGAGCT-----GACAGAAA	3222
Db	3953	CAGATAGTCTTGCCGCATCTTGGCAAGTTGCAGAGATGGTGGAGCTAGAAAAAAAAAAAAA	4012
Qy	3223	TAACCCCTTTTCACAGTTTGTGCACTGTGTACGGTCTGTGTAGGTTGATGCAGATTTTCTG	3282
Db	4013	AAAAGCCCTTTTTCAGTTTGTGCACTGTGTATGGTCCGTGTAGATTGATGCAGATTTTCTG	4072
Qy	3283	AAATGAAA----TGTTTAGACGAGATCATGCCACCAAGGCAGGAGTGAAAAAGCTTGCCT	3338
Db	4073	AAATGAAATGTTTGTTTAGACGAGATCATACCGGTAAAGCAGGAATGACAAAGCTTG-CT	4131
Qy	3339	TTCCTGGTATGTTCTAGGTGTATTGTGAAATTTACTGTTGTATTAATTGCCAATATAAGT	3398
Db	4132	TTTCTGGTATGTTCTAGGTGTATTGTGACTTTTACTGTTATATTAATTGCCAATATAAGT	4191
Qy	3399	AAATATAGATTATATATATCTATATATAGTGTTCACGAAGCTTAGCCCTTTACCTTCCC	3458
Db	4192	AAATATAGATTATATATG-----TATAGTGTTCACAAAGCTTAGACCTTTACCTT-CC	4244
Qy	3459	AGCTGCCCCACAGTGCTTGATACT-----TCTGTCATGGGTTTTATGTGTGTAGTCCCA	3512
Db	4245	AGCCACCCACAGTGCTTGATATTTTCAGAGTCAGTCATTGGTTATACATGTGTAGTTCCA	4304
Qy	3513	AAGCACATAAGCTAGGGAGAAACGTACTTCTAGGCGCACTACCATCTGTTTTCAACACGA	3572
Db	4305	AAGCACATAAGCTAGAAGAAGAAATATTTCTAGGAGCACTACCATCTGTTTTCAACATGA	4364
Qy	3573	ACCGACGCCATGCAAACAGAACTCC-TCAACATAAACTTCACTGCACAGACTTACTGTAG	3631
Db	4365	A---ATGCCACACACATAGAACTCCAACAACATCAATTTTCATTGCACAGACTGACTGTAG	4421
Qy	3632	TTAATTTTATCAC--AAACTCTGGACTGAATCTAATGCTTCCAAAAA-----TGTTTG	3682
Db	4422	TTAATTTTGTACAGAATCTATGGACTGAATCTAATGCTTCCAAAAATGTTGTTTGTTTG	4481
Qy	3683	CAAATATCAAACATTGTTATGTAAGAAAATAT-----AAATGACGATTTTATACAATT	3734
Db	4482	CAAATATCAAACATTGTTATGCAAGAAATTATTAATTACAAAATGAAGATTTATACCATT	4541
Qy	3735	GTGGTTTAAGCTGTATTGAACTAAATCTGTGGAATGCATTGTGAACTGTAAAAGCAAAGT	3794
Db	4542	GTGGTTTAAGCTGTACTGAACTAAATCTGTGGAATGCATTGTGAACTGTAAAAGCAAAGT	4601
Qy	3795	ATCAATAAAGCTTATAGACTTAAAAAAAAAAAA 3825	
Db	4602	ATCAATAAAGCTTATAGACTTAAAAAAAAAAAA 4632	

ID ABX34563 standard; cDNA; 4698 BP.
XX
AC ABX34563;
XX
DT 13-FEB-2003 (first entry)
XX
DE Human mddt cDNA SEQ ID 124.
XX
KW MDDT; human; disease detection and treatment molecule polypeptide;
KW anti-inflammatory; immunosuppressive; osteopathic; cytostatic; anti-HIV;
KW haemostatic; nephrotropic; antianaemic; antipsoriatic; hepatotropic;
KW gene therapy; protein replacement therapy; cell proliferative disorder;
KW cancer; adenocarcinoma; leukaemia; lymphoma; melanoma; myeloma; sarcoma;
KW anaemia; Crohn's disease; acquired immunodeficiency syndrome; AIDS;
KW Goodpasture's syndrome; inflammation; osteoporosis; thrombocytopaenia;
KW psoriasis; hepatitis; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200279449-A2.
XX
PD 10-OCT-2002.
XX
PF 27-MAR-2002; 2002WO-US09944.
XX
PR 28-MAR-2001; 2001US-279619P.
PR 29-MAR-2001; 2001US-280067P.
PR 29-MAR-2001; 2001US-280068P.
PR 16-MAY-2001; 2001US-291280P.
PR 17-MAY-2001; 2001US-291829P.
PR 17-MAY-2001; 2001US-291849P.
PR 19-JUN-2001; 2001US-299428P.
PR 20-JUN-2001; 2001US-299776P.
PR 20-JUN-2001; 2001US-300001P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;
PI Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshey SR;
PI Daugherty SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin EH;
PI Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;
PI Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;
XX
DR WPI; 2003-058431/05.
DR P-PSDB; ABU11573.
XX
PT New purified disease detection and treatment molecule proteins and
PT polynucleotides, useful for diagnosing, treating or preventing cancers
PT (e.g. leukemia or sarcoma), anemia, Crohn's disease, AIDS, osteoporosis
PT or hepatitis -
XX
PS Claim 1; SEQ ID NO 124; 339pp + Sequence Listing; English.
XX
CC This invention describes a novel disease detection and treatment molecule
CC polypeptide (MDDT) which has anti-inflammatory, immunosuppressive,
CC osteopathic, cytostatic, anti-HIV, haemostatic, nephrotropic,
CC antianaemic, antipsoriatic and hepatotropic activity. The polynucleotides

CC and the polypeptides of the invention can be used for gene therapy,
CC protein replacement therapy and are useful for treating a variety of
CC diseases or conditions. These polypeptides or polynucleotides are
CC particularly useful for diagnosing, treating or preventing cell
CC proliferative disorders (e.g. cancers including adenocarcinoma,
CC leukaemia, lymphoma, melanoma, myeloma or sarcoma), anaemia, Crohn's
CC disease, acquired immunodeficiency syndrome (AIDS), Goodpasture's
CC syndromes, inflammation, osteoporosis, thrombocytopaenia, psoriasis or
CC hepatitis. ABX34440-ABX34835 encode the MDDT polypeptides represented in
CC ABU11450-ABU11845, described in the disclosure of the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC o.int/pub/published_pct_sequences.

XX

SQ Sequence 4698 BP; 1410 A; 1028 C; 1022 G; 1238 T; 0 other;

Query Match 67.0%; Score 2566.4; DB 25; Length 4698;
Best Local Similarity 84.7%; Pred. No. 0;
Matches 3221; Conservative 0; Mismatches 441; Indels 140; Gaps 25;

```
Qy      1 CTATCTCCTCTCTCAGCCGCTGCTTTTAAAGAACGTGAATACCTTGGTGATTACAGCA 60
      || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      856 CTGTCTCCTCTCTCAGCCGCTTCTTCAAAGAACATGAATACCTTGGTAATTTGTCAACA 915

Qy      61 GTACTGCCCCACTGAAGGAACACTTCCAG-CAACTTCAAATGAAGCTTCTAAAGCATTCTC 119
      ||| | ||||| ||||| ||||| || || || ||||| ||||| ||||| |||||
Db      916 GTATTACCCACTGAAGGAACACTTCAAGAAAAATGTCAGTGAAGCTTCTAAAGAGGTCTC 975

Qy      120 AGAGAAGGCCAAAAATCCATTTGTAGAGAGAAATTTAAACAGAATTTTCAGAATTGGAATA 179
      ||||| ||||| || || || ||||| ||||| ||||| ||||| ||||| |||||
Db      976 AGAGAAGGCCAAAACTCTACTCATAGATAGAGATTTAAACAGAGTTTTCAGAATTAGAATA 1035

Qy      180 TTCAGAAATGGAATCATCATTTCAGTGGCTCTCAAAAGGCAGAACCTGCCGTAACAGTAGC 239
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1036 CTCAGAAATGGGATCATCGTTCAGTGTCTCTCCAAAAGCAGAAATCTGCCGTAATAGTAGC 1095

Qy      240 GAATCCTAGGGACGAAATAGTTGTGAGGAGTAGAGATAAAGAAGAGGACTTAGTTAGTCT 299
      ||||| ||||| ||||| ||||| || || || ||||| ||||| ||||| |||||
Db      1096 AAATCCTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGTTAGTTAGTAA 1155

Qy      300 TAACATCCTTCATACTCAGCAGGAGTTATCTACAGTCCTTACGAAATCAGTTGAAGAAGA 359
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1156 TAACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGA 1215

Qy      360 AGATAGAGTTCTGTCTCCAGAAAAAACAAGGACAGTTTTTAAGGAAAAGGGAGTTGCAGC 419
      || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1216 TGA---AGTTGTGTCTTCAGAAAAAGCAAAAGACAGTTTTTAATGAAAAGAGAGTTGCAGT 1272

Qy      420 AGAAGCTTCTATGGGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGT 479
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1273 GGAAGCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGT 1332

Qy      480 GAAAGATACTTACAAGCAAGATAGTGATGTTTTGATTGCTGGAGGTAATATAGAGAGCAA 539
      ||||| || || ||||| ||||| || || ||||| ||||| || ||||| |||||
Db      1333 GAAAGATAGT---AAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAAATCGAGAGCAA 1389

Qy      540 ATTGGAAGGTAAAGTGGATAAGAAACACTTTTCAGATAGCCTTGAACAAACAAATCGTGA 599
```

Db	1390	CTTGGAAGTAAAGTGGATAAAAAATGTTTTGCAGATAGCCTTGAGCAAATAATCACGA	1449
Qy	600	AAAAGATAGTGAAAGCAGTAATGATGACACTTCATTTCCCAGTACACCAGAAGCTGTAAG	659
Db	1450	AAAAGATAGTGAGAGTAGTAATGATGATACTTCTTTCCCCAGTACGCCAGAAGGTATAAA	1509
Qy	660	AGGTGGTTCGGAGCGTACATCACGTGTGCTCCCTTTAACC---CAACAAGTGAAGTGT	716
Db	1510	GGATCGTTTCAGGAGCATATATCACATGTGCTCCCTTTAACCAGCAGCAACTGAGAGCAT	1569
Qy	717	TTCAACAAACATTTTTCCCTTGTGGAAGATCATACTTCGGAAAATAAGACAGATGAAAA	776
Db	1570	TGCAACAAACATTTTTCTTTGTAGGAGATCTTACTTCAGAAAATAAGACCGATGAAAA	1629
Qy	4377	-AAAAAAGGCACAAATTGTAACAGAGAAGAATGCAAGTGTCAAGACATC	835
Db	1630	AAAAATAGAAGAAAAGAAGGCCAAATAGTAACAGAGAAGAATACTAGCACCAAAACATC	1689
Qy	836	AAACCCTTTCCTTATGGCAGCACAGGAGTCTAAGACAGATTACGTTACAACAGATCATGT	895
Db	1690	AAACCCTTTCCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATTT	1749
Qy	896	GTCAAAGGTGACCGAGGAAGTAGTGGCAAACATGCCTGAAGGTCTAACCCCAGATTTGGT	955
Db	1750	AACAAAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGT	1809
Qy	956	TCAGGAAGCATGTGAAAGTGAATTGAATGAAGCTACTGGTACAAAAATTGCCTTTGAAAC	1015
Db	1810	ACAGGAAGCATGTGAAAGTGAATTGAATGAAGTACTGGTACAAAGATTGCTTA GAAAC	1869
Qy	1016	AAAAATGGACCTGGTTCAAACCTCAGAAGCTGTGCAGGAGTCACTTTACCTGTAAACACA	1075
Db	1870	AAAAATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACA	1929
Qy	1076	GCTTTGCCCATCTTTTGAAGAATCTGAAGCTACTCCGTACCCGGTTTTGCCTGACATTGT	1135
Db	1930	GCTTTGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTACCAGTTTTGCCTGACATTGT	1989
Qy	1136	CATGGAAGCACCATTAAATTCGTAGTTCCTAGTGCTGGTGCTTCTGCAGTGCAGCTCAG	1195
Db	1990	TATGGAAGCACCATTGAATTCGTAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCAG	2049
Qy	1196	TTCATCACCATTAGAACTCTTCCTTCAGTTAATTATGAAAGCATAAAGTTTGAGCCTGA	1255
Db	2056	ATTATGAAAGCATAAAACATGAGCCTGA	2106
Qy	1256	AAATCCCCCACCATATGAGGAGGCCATGAATGTATCACTAAAAAAGAATCAGGAATGAA	1315
Db	2107	AAACCCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAA	2166
Qy	1316	TGAAGAAATCACAGAGCCTGAAGGTATTAGTGTAGCTGTTTCAGGAAACAGAAGCTCCTTA	1375
Db	2167	GGAAGAAATTAAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTA	2226
Qy	1376	TATATCTATTGCATGTGATTTAATTAAAGAAACAAAGATCTCTACTGAACCGACTCCAGA	1435

Db	2227	TATATCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCAGCTCCGGA	2286
Qy	1436	TTTCTCTAGTTATTCAGAAATAGCAGAAGTTGCACAGCCAGTGCCCGAGCATTCTGAGCT	1495
Db	2287	TTTCTCTGATTATTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCT	2346
Qy	1496	AGTTGAAGATTCTCTCCCCGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACC	1555
Db	2347	AGTTGAAGATTCTCTACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACC	2406
Qy	1556	CGAAGTTCCACAAAAACAAGATGAAGCTGTAATACTTGTGAAAGAAAACTCACTGAAAT	1615
Db	2407	TGACGTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGAC	2466
Qy	1616	TTCATCTGAGTCAATGACAGGACATGACAATAAGGGAAAACTCAGTGCTTCACCATCACC	1675
		b4\$47\$Xt	
Db	2467	TTCATTTGAGTCAATGATAGAATATGAAAATAAGGAAAACTCAGTGCTTTTGC---CACC	2523
Qy	1676	TGAGGGAGGAAAAACCGTATTTGGAGTCTTTTCAGCCCAGTTTAGGCATCACAAAAGATAC	1735
Db	2524	TGAGGGAGGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATAC	2583
Qy	1736	CTTAGCACCTGATGAAGTTTCAGCATTGACCCAAAAGGAGAAAAATCCCTTTGCAGATGGA	1795
Db	2584	CCTGTTACCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAATTCCTTTGCAGATGGA	2643
Qy	1796	GGAGCTCAATACTGCAGTTTATTCAAGTGATGGCTTATTCATTGCTCAGGAAGCAAACCT	1855
Db	2644	GGAGCTCAGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGAT	2703
Qy	1856	AAGAGAAAGTGAAACATTTTCAGATTTCATCTCCGATTGAGATT TAGATGAGTTCCCGAC	1915
Db	2704	AAGAGAAACTGAAACGTTTTCAGATTTCATCTCCAATTGAAATTATAGATGAGTTCCCTAC	2763
Qy	1916	CTTTGTGAGTTCTAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACACTGACCTAGA	1975
Db	2764	ATTGATCAGTTCTAAAACTGATTCATTTTCTAAATTAGCCAGGGAATATACTGACCTAGA	2823
Qy	1976	AGTAGCCACAAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTCATTGGCTTGTGC	2035
Db	2824	AGTATCCACAAAAGTGAAATTGCTAATGCCCGGATGGAGCTGGGTCATTGCCTTGCAC	2883
Qy	2036	AGGATTGCCCCATGACCTTTCTTTCAAGAGTATACAACC-----TAAAGAGGAAGTTCA	2089
Db	2884	AGAATTGCCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAG	2943
Qy	2090	TGTCCCAGAT	
Db	2944	TTTCTCAGATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCC	3003
Qy	2150	AGATGTTTCTGCTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAAACCCAAAGTTCT	2209
Db	3004	AGATGTTTCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCT	3063
Qy	2210	TGTGAAAGAAGCCGAGAGAAAACTTCCTTCTGATACAGAAAAAGAGCGAAGATCTCCATC	2269
		GATA0000T0AT0TTTCAAA00T0CCC0TACT000T00 20X0	
Db	3064	TGTGAAAGAAGCTGAGAAAAAATTCCTTCCGATACAGAAAAAGAGGACAGATCACCATC	3123

Qy	2270	TGCTATATTTTCAGCAGAGCTGAGTAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGA	2329
Db	3124	TGCTATATTTTCAGCAGAGCTGAGTAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGA	3183
Qy	2330	CATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTGTTCCCTGCTGCTCTCGCTGACAGT	2389
Db	3184	CATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTCCTGCTGCTTTCATTGACAGT	3243
Qy	2390	ATTCAGCATTGTGAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCTGTGACTATCAG	2449
Db	3244	ATTCAGCATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAG	3303
Qy	2450	CTTTAGGATATATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATT	2509
Db	3304	TATCTAGGACTACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATT	3363
Qy	2510	CAGGGCATATTTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGCAA	2569
Db	3364	CAGGGCATATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAA	3423
Qy	2570	TTCTGCTCTTGGTCATGTTAACTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGTTGA	2629
Db	3424	TTCTGCTCTTGGTCATGTGAAGTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGA	3483
Qy	2630	TGATTTAGTTGATTCTCTGAAGTTTGAGTGTGATGTGGGTATTTACCTATGTTGGTGC	2689
Db	3484	TGATTTAGTTGATTCTCTGAAGTTTGAGTGTGATGTGGGTATTTACCTATGTTGGTGC	3543
Qy	2690	CTTGTTCAATGGTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCCTGT	2749
Db	3544	CTTGTTTAATGGTCTGACACTACTGATTTTGGCTCTCATTTCCTTCAGTGTTCCTGT	3603
Qy	2750	TATTTATGAACGGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGT	2809
Db	3604	TATTTATGAACGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATAAGAATGT	3663
Qy	2810	TAAAGATGCTATGGCTAAATCCAAGCAAAATCCCTGGATTGAAGCGTAAAGCTGAATG	2869
Db	3664	TAAAGATGCTATGGCTAAATCCAAGCAAAATCCCTGGATTGAAGCGCAAAGCTGAATG	3723
Qy	2870	AGAAAGCCTGAAAGAGTTAAACAATAGAGGAGTTTATCTTTAAAGGGGATATTCATTTGAT	2929
Db	3724	AAAACGCCCAAATAATTA-----GTAGGAGTTCATCTTTAAAGGGGATATTCATTTGA-	3777
Qy	2930	TCCATTGGGGAGGGTCAGGGAAGAACAAGCCTTGACATTGCAGTGCAGTTTCACAGATC	2989
		60/03 6215X:	
Db	3778	-----TTATACGGATC	3788
Qy	2990	TTTATTTTGTAGCAACGCAGTG-TCTGAGGAAAAATGACCTGTCTTGACTGCCCTGTGTTT	3048
Db	3789	TTTATTTTGTAGCCATGCACTGTTGTGAGGAAAAATACCTGTCTTGACTGCCATGTGTTT	3848
Qy	3049	ATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTTAAATCGTAATCATATTTGTTTTT	3108
Db	3849	ATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTTAAACCGTAATCATA--TCTTTTT	3906

Qy	3109	CCTGTATGAGGCACTGGTGAATAAAACAAAGATCTGAGAAAGCTGTATATTACACTTTGTC	3168
Db	3907	CCTATCTGAGGCACTGGTGGA-----ATAAAAAACCTGTATATTTTACTTTGTT	3955
Qy	3169	GCAGGTAGTCTTGCTGTAT-TTGGGGAATTGCAAAGAAAGTGGAGCT-----GACAG	3219
Db	3956	GCAGATAGTCTTGCCGCATCTTGCCAAGTTGCAGAGATGGTGGAGCTAGAAAAAAAAG	4015
Qy	3220	AAATAACCCCTTTTCACAGTTTGTGCACTGTGTACGGTCTGTGTAGGTTGATGCAGATTTT	3279
Db	4016	AAAAAAGCCCTTTTCAGTTTGTGCACTGTGTATGGTCCGTGTAGATTGATGCAGATTTT	4075
Qy	3280	CTGAAATGAAA----TGTTTAGACGAGATCATGCCACCAAGGCAGGAGTGAAAAAGCTTG	3335
Db	50X 6	CTGAAATGAAATGTTTGTGTACGAGATCATACCGGTAAAGCAGGAATGACAAAGCTTG	4135
Qy	3336	CCTTTCCTGGTATGTTCTAGGTGTATTGTGAAATTTACTGTTGTATTAATTGCCAATATA	3395
Db	4136	-CTTTCCTGGTATGTTCTAGGTGTATTGTGACTTTTACTGTTATATTAATTGCCAATATA	4194
Qy	3396	AGTAAATATAGATTATATATATCTATATATAGTGTTTCACGAAGCTTAGCCCTTTACCTT	3455
Db	4195	AGTAAATATAGATTATA-----TATGTATAGTGTTTCACAAAGCTTAGACCTTTACCTT	4248
Qy	3456	CCCAGCTGCCCCACAGTGCTTGATACT-----TCGTGCATGGGTTTTATGTGTGTAGTC	3509
Db	4249	-CCAGCCACCCACAGTGCTTGATATTTTCAGAGTCAGTCATTGGTTATACATGTGTAGTT	4307
Qy	3510	CCAAAGCACATAAGCTAGGGAGAAACGTACTTCTAGGCGCACTACCATCTGTTTTCAACA	3569
		/0	
Db	4308	CCAAAGCACATAAGCTAGAAGAAGAAATATTTCTAGGAGCACTACCATCTGTTTTCAACA	4367
Qy	3570	CGAACCGACGCCATGCAAACAGAACTCC-TCAACATAAACTTCACTGCACAGACTTACTG	3628
Db	4368	TGAA---ATGCCACACACATAGAACTCCAACAACATCAATTTTCATTGCACAGACTGACTG	4424
Qy	3629	TAGTTAATTTTATCAC--AAACTCTGGACTGAATCTAATGCTTCCAAAAA-----TGT	3679
Db	4425	TAGTTAATTTTGTACAGAATCTATGGACTGAATCTAATGCTTCCAAAAATGTTGTTTGT	4484
Qy	3680	TTGCAAATATCAAACATTGTTATGTAAGAAAATAT-----AAATGACGATTTTATACA	3731
Db	4485	TTGCAAATATCAAACATTGTTATGCAAGAAATTATTAATTACAAAATGAAGATTTATACC	4544
Qy	3732	ATTGTGGTTTAAAGCTGTATTGA	3753
D	5	ATGGTAGCTTAAGCTGTACTGA	4566

RESULT 5

AAS09453

ID AAS09453 standard; cDNA; 4053 BP.

XX

AC AAS09453;

XX

DT 26-SEP-2001 (first entry)

XX

DE Human cDNA encoding the Nogo protein.

XX

KW Human; Nogo receptor; axonal growth; immunogen; antibody; nogo protein;
KW cranial trauma; cerebral trauma; spinal cord injury; stroke;
KW demyelinating disease; multiple sclerosis; monophasis demyelination;
KW encephalomyelitis; multifocal leukoencephalopathy; panencephalitis;
KW Marchiafava-Bignami disease; pontine myelinolysis; adrenoleukodystrophy;
KW Pelizaeus-Merzbacher disease; Spongy degeneration; Alexander's disease;
KW Canavan's disease; metachromatic leukodystrophy; viral infection;
KW Krabbe's disease; AB020693; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers
FT CDS 135..3713
FT /*tag= a
FT /product= "Nogo protein"

XX

PN WO200151520-A2.

XX

PD 19-JUL-2001.

XX

PF 12-JAN-2001; 2001WO-US01041 2

XX

PR 12-JAN-2000; 2000US-0175707.
PR 26-MAY-2000; 2000US-0207366.
PR 29-SEP-2000; 2000US-0236378.

XX

PA (UYYA) UNIV YALE.

XX

PI Strittmatter SM;

XX

DR WPI; 2001-442138/47.
DR P-PSDB; AAU09453.

XX

PT Novel Nogo receptor protein useful for identifying modulator of Nogo
PT protein or Nogo receptor protein, which is useful for treating central
PT nervous system disorders -

XX

PS Example 1; Page 95-100; 109pp; English.

XX

CC The sequence (Genbank accession number AB0202693) encodes the human Nogo
CC protein, a 250kDa myelin-associated axon growth inhibitor. The invention
CC relates to the use of the nogo receptor, nogo protein, their nucleic
CC acids, vectors expressing them and antibodies against them, to isolate
CC agents which block nogo receptor mediated axonal growth. The agent is
CC useful for treating a central nervous system disorder which is a result
CC of cranial or cerebral trauma, spinal cord injury, stroke or a
CC demyelinating disease selected from multiple sclerosis, monophasis
CC demyelination, encephalomyelitis, multifocal leukoencephalopathy,
CC panencephalitis, Marchiafava-Bignami disease, pontine myelinolysis,
CC adrenoleukodystrophy, Pelizaeus-Merzbacher disease, Spongy degeneration,
CC Alexander's disease, Canavan's disease, metachromatic leukodystrophy,
CC viral infection and Krabbe's disease.

XX

SQ Sequence 4053 BP; 1189 A; 922 C; 922 G; 1020 T; 0 other;

Query Match 62.1%; Score 2379.4; DB 22; Length 4053;
Best Local Similarity 86.6%; Pred. No. 0;
Matches 2802; Conservative 0; Mismatches 381; Indels 54; Gaps 14;

```
Qy      1 CTATCTCCTCTCTCAGCCGCTGCTTTTAAAGAACGTGAATACCTTGGTGATTTACCAGCA 60
      || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    846 CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAATTTGTCAACA 905

Qy     61 GTACTGCCCACTGAAGGAACACTTCCAGCAACTTCAAATGAAGCTTCTAAAGCATTCTCA 120
      ||| | ||||| ||||| ||||| || ||| | ||||| ||||| ||||| |||||
Db    906 GTATTACCCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA 965

Qy    121 GAGAAGGCAAAAAATCCATTTGTAGAGAGAAAATTTAACAGAATTTTCAGAATTGGAATAT 180
      ||||| ||||| || ||| ||||| ||||| ||||| ||||| ||||| |||||
Db    966 GAGADGCEAAAATCTCTACTCATAGATAGAGATTTAACAGAGTTTT          AATAC 1025

Qy    181 TCAGAAATGGAATCATCATTCAGTGGCTCTCAAAAGGCAGAACCTGCCGTAACAGTAGCG 240
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   1026 TCAGAAATGGGATCATCGTTCAGTGTCTCTCCAAAAGCAGAATCTGCCGTAATAGTAGCA 1085

Qy    241 AATCCTAGGGACGAAATAGTTGTGAGGAGTAGAGATAAAGAAGAGGACTTAGTTAGTCTT 300
      ||||| ||||| ||||| || ||| || ||||| ||||| ||||| ||||| |||||
Db   1086 AATCCTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGTTAGTTAGTAAT 1145

Qy    301 AACATCCTTCATACTCAGCAGGAGTTATCTACAGTCCTTACGAAATCAGTTGAAGAAGAA 360
      ||||| ||||| || ||| ||||| ||||| ||||| ||||| ||||| |||||
Db   1146 AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT 1205

Qy    361 GATAGAGTTCTGTCTCCAGAAAAAACAAAGGACAGTTTTAAGGAAAAGGGAGTTGCAGCA 420
      || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   1206 GAG-DAGTGTGTCTTCAG          AAGACAGTTTTAATGAAAAGAGAGTTGCAGTG 1262

Qy    421 GAAGCTTCTATGGGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG 480
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   1263 GAAGCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG 1322

Qy    481 AAAGATACTTACAAGCAAGATAGTGATGTTTTGATTGCTGGAGGTAATATAGAGAGCAAA 540
      ||||| || ||| ||||| ||||| || ||| ||||| ||||| ||||| |||||
Db   1323 AAAGATAGT---AAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAAATCGAGAGCAAC 1379

Qy    541 TTGGAAGGTAAAGTGGATAAGAAACACTTTTTCAGATAGCCTTGAACAAACAAATCGTGAA 600
      ||||| ||||| ||||| ||||| || ||| ||||| ||||| ||||| |||||
Db   1380 TTGGAAGGTAAAGTGGATAAAAAATGTTTTGCAGATAGCCTTGAACAAACTAATCACGAA 1439

Qy    601 AAAGATAGTGAAAGCAGTAATGATGACACTTCATTTCCCAGTACACCAGAAGCTGTAAGA 660
      ||||| ||||| || ||||| ||||| ||||| || ||||| ||||| ||||| |||||
Db      0 AAAGATACTGAGAGTGTAGTAATGATGATACCTTCTTTCCCAGTACGCCAGAAGGTATAAAG 1499

Qy    661 GGTGGTTCCGGAGCGTACATCACGTGTGCTCCCTTTAACC---CAACAACCTGAGAATGTT 717
      || ||||| ||||| || ||||| ||||| ||||| ||||| ||||| |||||
Db   1500 GATCGTTTCAGGAGCATATATCACATGTGCTCCCTTTAACCCAGCAGCAACTGAGAGCATT 1559

Qy    718 TCAACAAACATTTTTCCCTTGTTGGAAGATCACTTCCGAAAAATAAGACAGATGAAAAA 777
      ||||| ||||| ||||| || ||||| ||||| ||||| ||||| ||||| |||||
Db   1560 GCAACAAACATTTTTCCTTTGTTAGGAGATCCTACTTCAGAAAAATAAGACCGATGAAAAA 1619

Qy    778 AAGATAGAA-AAAAAAGGCACAAATTGTAACAGAGAAGAATGCAAGTGTCAAGACATCA 836
```

Db	1620	<pre> AAAA TAGAAGAAAAGAAGGCCAAATAGTAACAGAGAAGAATACTAGCACCAAACATCA </pre>	1679
Qy	837	<pre> AACCCTTTCTTATGGCAGCACAGGAGTCTAAGACAGATTACGTTACAACAGATCATGTG </pre>	896
Db	1680	<pre> AACCCTTTCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATTTA </pre>	1739
Qy	897	<pre> TCAAAGGTGACCGAGGAAGTAGTGGCAAACATGCCTGAAGGTCTAACCCAGATTTGGTT </pre>	956
Db	1740	<pre> ACAAAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTA </pre>	1799
Qy	957	<pre> CAGGAAGCATGTGAAAGTGAATTGAATGAAGCTACTGGTACAAAATTGCCTTTGAAACA </pre>	1016
Db	1800	<pre> CAGGAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACA </pre>	1859
Qy	1017	<pre> A7G DATE: TGGTTCAAACCTTCAGAAGCTGTGCAGGAGTCACTTTACCCTGTAACACAG </pre>	1076
Db	1860	<pre> AAAATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAG </pre>	1919
Qy	1077	<pre> CTTTGCCCATCTTTTGAAGAATCTGAAGCTACTCCGTCAACGGTTTTGCCTGACATTGTC </pre>	1136
Db	1920	<pre> CTTTGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGCCTGACATTGTT </pre>	1979
Qy	1137	<pre> ATGGAAGCACCATTAAATTCTGTAGTTCCTAGTGCTGGTGCTTCTGCAGTGCAGCTCAGT </pre>	1196
Db	1980	<pre> ATGGAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCAGC </pre>	2039
Qy	1197	<pre> TCATCACCATTAGAACTCTTCCTTCAGTTAATTATGAAAGCATAAAGTTTGAGCCTGAA </pre>	1256
Db	2040	<pre> TCATCACCATTAGAAGC---TTCTTCAGTTAATTATGAAAGCATAAAACATG GCTGAA </pre>	2096
Qy	1257	<pre> AATCCCCCACCATATGAGGAGGCCATGAATGTATCACTAAAAAAGAATCAGGAATGAAT </pre>	1316
Db	2097	<pre> AATCCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAG </pre>	2156
Qy	1317	<pre> GAAGAAATCACAGAGCCTGAAGGTATTAGTGTAGCTGTTTCAAGAAACAGAAGCTCCTTAT </pre>	1376
Db	2157	<pre> GAAGAAATTAAGAGCCTGAAAAATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTAT </pre>	2216
Qy	1377	<pre> ATATCTATTGCATGTGATTTAATTAAAGAAACAAAGATCTCTACTGAACCGACTCCAGAT </pre>	1436
Db	2217	<pre> ATATCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCAGCTCCGGAT </pre>	2276
Qy	1437	<pre> TTCTCTAGTTATTCAGAAATAGCAGAAGTTGCACAGCCAGTGCCCCGAGCATTCTGAGCTA </pre>	1496
Db	2277	<pre> TTCTCTGATTATTCAGAAATGGCT CAGCCAGTGCCTGATCATTCAAGAGTGA </pre>	2336
Qy	1497	<pre> GTTGAAGATTCTCCCCGATTCTGAACCAAGTTGACTTATTTAGTGATGATTCAATACCC </pre>	1556
Db	2337	<pre> GTTGAAGATTCTCACCTGATTCTGAACCAAGTTGACTTATTTAGTGATGATTCAATACCT </pre>	2396
Qy	1557	<pre> GAAGTTCCACAAAAACAAGATGAAGCTGTAATACTTGTGAAAGAAAACCTCACTGAAATT </pre>	1616
Db	2397	<pre> GACGTTCCACAAAAACAAGATGAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACT </pre>	2456
Qy	1617	<pre> TCATCTGAGTCAATGACAGGACATGACAATAAGGGAAAACTCAGTGCTTCACCATCACCT </pre>	1676

Db	2457	TCATTTGAGTCAATGATAGAAATATGAAAAAATAAGGAAAAAACTCAGTGCTTTGCG---CACCT	2513
Qy	1677	GAGGGAGGAAAAACCGTATTTGGAGTCTTTTCAGCCCAGTTTAGGCATCACAAAAGATAACC	1736
Db	2514	GAGGGAGGAAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATAACC	2573
Qy	1737	TTAGCACCTGATGAAGTTTCAGCATTGACCCAAAAGGAGAAAAATCCCTTTGCGAGATGGAG	1796
Db	2574	CTGTTACCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAAATTCCTTTGCGAGATGGAG	2633
Qy	1797	GAGCTCAATACTGCAGTTTATTCAAGTGATGGCTTATTCAATTGCTCAGGAAGCAAACCTA	1856
Db	2634	GAGCTCAGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATA	2693
Qy	1857	AGAGAAAAGTGAAAACATTTTCAGATTTCATCTCCGATTGAGATTATAGATGAGTTCCCGACC	1916
Db	2694	AGAGAAAAGTGAAAACGTTTTCAGATTTCATCTCCAATTGAAATTATAGATGAGTTCCCTACA	2753
Qy	1917	TTTGTTCAGTTCTAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACACTGACCTAGAA	1976
Db	2754	TTGATCAGTTCTAAAAGTATTCAATTTCTAAATTAGCCAGGGAATATACTGACCTAGAA	2813
Qy	1977	GTAGCCCACAAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTTCATTGGCTTGTGCA	2036
Db	2814	GTATCCCACAAAAGTGAAATTGCTAATGCCCGGATGGAGCTGGGTTCATTGCCTTGCACA	2873
Qy	2037	GGATTGCCCATGACCTTTCTTTCAAGAGTATACAACC-----TAAAGAGGAAGTTCAT	2090
Db	2874	GAATTGCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGT	2933
Qy	2091	GTCCCGATGAGTTCTCCAAAGATAGGGGTGATGTTTCAAAGGTGCCCGTACTGCCTCCA	2150
Db	2934	TTCTCAGATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCA	2993
Qy	2151	GATGTTTCTGCTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAAACCCAAAGTTCTT	2210
Db	2994	GATGTTTCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTT	3053
Qy	2211	GTGAAAGAAGCCGAGAGAAAACTTCCTTCTGATACAGAAAAAGAGCGAAGATCTCCATCT	2270
Db	3054	GTGAAAGAAGCTGAGTGAAGAAAAATCTTGGTCTCCATCTCTGATGAGGAGGATGAGATCT	3113
Qy	2271	GCTATATTTTCAGCAGAGCTGAGTAAAACCTCAGTTGTTGACCTCCTCTACTGGAGAGAC	2330
Db	3114	GCTATATTTTCAGCAGAGCTGAGTAAAACCTCAGTTGTTGACCTCCTGTACTGGAGAGAC	3173
Qy	2331	ATTAAGAAGA	
Db	3174	ATTAAGAAGACTGGAGTGGTGTTGGTGCCAGCCTATTCTGCTGCTTTTCATTGACAGTA	3233
Qy	2391	TTCAGCATTGTGAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCTGTGACTATCAGC	2450
Db	3234	TTCAGCATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGC	3293
Qy	2451	TTTAGGATATATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATTC	2510
Db	3294	TTTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTC	3353

Qy	2511	AGGGCATATTTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTTCAGAAGTACAGCAAT	2570
Db	3354	AGGGCATATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTTCAGAAGTACAGTAAT	3413
Qy	2571	TCTGCTCTTGGTCATGTAACTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGTTGAT	2630
Db	3414	TCTGCTCTTGGTCATGTGAAGTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGAT	3473
Qy	2631	GATTTAGTTGATTCTCTGAAGTTTGAGTGTGGGTATTTACCTATGTTGGTGCC	2690
Db	3474	GATTTAGTTGATTCTCTGAAGTTTGAGTGTGGGTATTTACCTATGTTGGTGCC	3533
Qy	2691	TTGTTCAATGGTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCCTGTT	2750
Db	353		
Qy	2751	ATTTATGAACGGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTT	2810
Db	3594	ATTTATGAACGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTT	3653
Qy	2811	AAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGAATGA	2890
Db	3654	AAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGAATGA	3713
Qy	2871	GAAAGCCTGAAAGAGTTAACAATAGAGGAGTTTATCTTTAAAGGGGATATTCATTTGATT	2930
Db	3714	AAACGCCCAAATAATTA-----GTAGGAGTTCATCTTTAAAGGGGATATTCATTTGATT	3768
Qy	2931	CCATTGGGGAGGGTCAGGGAAGAACAAGCCTTGACATTGCAGTGCAGTTTCAC-----	2984
Db	3769	ATACGGGGGAGGGTCAGGGAAGAACGAA-CCTTGACGTGCAGTGCAGTTTCACAGATCG	3827
Qy	2985	-----AGATCTTTATTTTGTAGCAACGCAGTG-TCTGAGGAAAAATGACCTGTCTTGACTG	3038
Db	3828	TTGTTAGATCTTTATTTTGTAGCCATGCACTGTTGTGAGGAAAAATTACCTGTCTTGACTG	3887
Qy	3039	CCCTGTGTTTCATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTAAATCGTAATCAT	3098
Db	3888	CCATGTGTTTCATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTAAACCGTAATCAT	3947
Qy	3099	ATTTGTTTTTCTGTATGAGGCACTGGTGAATAAAACAAAGATCTGAGAAAGCTGTATATT	3158
Db	3948	A--TCTTTTTCTATCTGAGGCACTGGTGA-----ATAAAAAACCTGTATATT	3994
Qy	3159	ACACTTTGTGCGAGGTAGTCTTGCTGTAT-TTGGGGAATTGCAAAGAAAGTGGAGCT	3214
Db	3995	TTACTTTGTTGCAGATAGTCTTGCCGCATCTTGGCAAGTTGCAGAGATGGTGGAGCT	4051

RESULT 6

AAA23454

ID AAA23454 standard; cDNA; 4093 BP.

XX

AC AAA23454;

XX

DT 19-JUN-2000 (first entry)

XX
DE cDNA encoding human secreted protein vb22_1, SEQ ID NO:63.
XX
KW Human; secreted protein; cancer; tumour; cardiovascular disorder;
KW blood disorder; haemophilia; autoimmune disease; diabetes; inflammation;
KW infection; fungal; bacterial; viral; HIV; allergy; arthritis;
KW neurodegenerative disease; asthma; contraceptive; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1048..3729
FT /*tag= a
FT /product= "Human secreted protein vb22_1"
FT CDS 152..1006
FT /*tag= b
FT /product= "Clone vb22_1 ORF2"
XX
PN WO200011015-A1.
XX
PD 02-MAR-2000.
XX
PF 24-AUG-1999; 99WO-US19351.
XX
PR 24-AUG-1998; 98US-0097638.
PR 24-AUG-1998; 98US-0097659.
PR 09-SEP-1998; 98US-0099610X
PR 28-SEP-1998; 98US-0102092.
PR 25-NOV-1998; 98US-0109978.
PR 23-DEC-1998; 98US-0113645.
PR 23-DEC-1998; 98US-0113646.
PR 23-AUG-1999; 99US-0379246.
XX
PA (ALPH-) ALPHAGENE INC.
XX
PI Valenzuela D, Yuan O, Hoffman H, Hall J, Rapiejko P;
XX
DR WPI; 2000-224657/19.
DR P-PSDB; AAY95012, AAY95030.
XX
PT New secreted or transmembrane proteins and polynucleotides encoding
PT them, useful for treating neurodegenerative disorders, autoimmune
PT diseases and cancer -
XX
PS Claim 72; Page 321-322; 357pp; English.
XX
CC The invention relates to 40 human secreted proteins (AAY94981-Y95020),
CC and cDNA sequences encoding them (AAA23423-A23462). The secreted
CC proteins of the invention include those that are thought to be only
CC partially secreted, i.e., transmembrane proteins. The proteins of the
CC in5XA on may exhibit 4 or more activities selected from the following:
CC cytokine activity; cell proliferation; differentiation; immune
CC modulation; haematopoiesis regulation; tissue growth activity;
CC activin/inhibin activity; chemotactic/chemokinetic activity; haemostatic
CC and thrombolytic activity; anti-inflammatory activity; and tumour
CC inhibition activity. The proteins may be administered to patients as
CC vaccines, and the nucleotides may be used as part of a gene therapy

Qy	541	TTGGAAGGTAAAGTGGATAAGAAACACTTTTCAGATAGCCTTGAACAAACAAATCGTGAA	600
Db	1396	TTGGAAAGTAAAGTGGATAAAAAATGTTTTGCAGATAGCCTTGAGCAAACATAATCACGAA	1455
Qy	601	AAAGATAGTGAAAGCAGTAATGATGACACTTCATTTCCCAGTACACCAGAAGCTGTAAGA	660
Db	1456	AAAGATAGTGAGAGTAGTAATGATGATACTTCTTTCCCCAGTACGCCAGAAGGTATAAAG	1515
Qy	661	GGTGGTTCCGGAGCGTACATCACGTGTGCTCCCTTTAACC--CAACAACAGAGAATGTT	717
Db	1516	GATCGTTTCCAGGAGCATATATCACATGTGCTCCCTTTAACCAGCAGCAACTGAGAGCATT	1575
Qy	718	TCAACAAACATTTTTCCTTGTGGAAGATCATACTTCGGAAAATAAGACAGATGAAAAA	777
Db	1576	GCAACAAACATTTTTCCTTGTGGAAGATCATACTTCGGAAAATAAGACCGATGAAAAA	1635
Qy	778	AAGATAGAA-AAAAAAGGCACAAATTGTAACAGAGAAGAATGCAAGTGTCAAGACATCA	836
Db	1636	AAAATAGAGAAAAGAAGGCCCAATAGTAACAGAGAAGAATACTAGCACCAAAACATCA	1695
Qy	837	AACCCCTTTCCTTATGGCAGCACAGGAGTCTAAGACAGATTACGTTACAACAGATCATGTG	896
Db	1696	AACCCCTTTCCTTATGGCAGCACAGGAGTCTAAGACAGATTACGTTACAACAGATCATTTA	1755
Qy	897	TCAAAGGTGACCGAGGAAGTAGTGGCAAACATGCCTGAAGGTCTAACCCAGATTGGTT	956
Db	1756	ACAAAGGTGACTGAGGAAGTTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTAGTA	1815
Qy	957	CAGGAAGCATGTGAAAGTGAATTGAATGAAGCTACTGGTACAAAAATTGCCTTTGAAACA	1016
Db	1816	CAGGAAGCATGTGAAAGTGAATTGAATGAAGTACTGGTACAAAGATTGCTTATGAAACA	1875
Qy	1017	AAAATGGACCTGGTTCAAACCTCAGAAGCTGTGCAGGAGTCACTTTACCTGTAACACAG	1076
Db	1876	AAAATGGACCTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAG	1935
Qy	1077	CTTTGCCCATCTTTTGAAGAATCTGAAGCTACTCCGTACCCGGTTTTGCCTGACATTGTC	1136
Db	1936	CTTTGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTACCAGTTTTGCCTGACATTGTT	1995
Qy	1137	ATGGAAGCACCATTAAATTCTGTAGTTCCTAGTGCTGGTGCTTCTGCAGTGCAGCTCAGT	1196
Db	1996	ATGGAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCAGC	2055
Qy	1197	TCATCACCATTAGAAACTCTTCCTTCAGTTAATTATGAAAGCATAAAGTTTGAGCCTGAA	1256
Db	2056	TCATCACCATTAGAAGCTT---CTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAA	2112
Qy	1257	AATCCCCCACCATATGAGGAGGCCATGAATGTATCACTAAAAAAGAATCAGGAATGAAT	1316
Db	2113	AATCCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAG	2172
Qy	1317	GAAGAAATCAGAGCCTGAAGGTATTAGTGTAGCTGTTTCAAGAAACAGAAGCTCCTTAT	1376
Db	2173	GAAGAAATTAAAGAGCCTGAAAAATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTAT	2232
Qy	1377	ATATCTATTGCATGTGATTTAATTAAAGAAACAAAGATCTCTACTGAACCGACTCCAGAT	1433

Db	2233	 ATATCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCAGCTCCGGAT	2292
Qy	1437	 TTCTCTAGTTATTTCAGAAATAGCAGAAAGTTGCACAGCCAGTGCCCGAGCATTCTGAGCTA	1496
Db	2293	 TTCTCTGATTATTTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCTA	2352
Qy	1497	 GTTGAAGATTCCCTCCCCGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCC	1556
Db	2353	 GTTGAAGATTCCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCT	2412
Qy	1557	 GAAGTTCCACAAAAACAAGATGAAGCTGTAATACTTGTGAAAGAAAACCTCACTGAAATT	1616
Db	2413	 GACGTTCCACAAAAACAAGATGAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACT	2472
Qy	1617	 TCATCTGAGTCAATGACAGGACATGACAATAAGGGAAAACTCAGTGCTTCACCATCACCT	1676
Db	2473	 TCATTTGAGTCAATGATAGAATATGAAAAAAGGAAAAAACTCAGTGCTTTGC---CACCT	2529
Qy	1677	 GAGGGAGGAAAACCGTATTTGGAGTCTTTTCAGCCCAGTTTAGGCATCACAAAAGATACC	1736
Db	2530	 GAGGGAGGAAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACC	2589
Qy	1737	 TTAGCACCTGATGAAGTTTCAGCATTGACCCAAAAGGAGAAAAATCCCTTTGCAGATGGAG	1796
Db	2590	 CTGTTACCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAAATTCCTTTGCAGATGGAG	2649
Qy	1797	 GAGCTCAATACTGCAGTTTATTCAAGTGATGGCTTATTCATTGCTCAGGAAGCAAACCTA	1856
Db	2650	 GAGCTCAGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATA	2709
Qy	1857	 AGAGAAAGTGAAACATTTTCAGATTTCATCTCCGATTGAGATTATAGATGAGTTCCCGACC	1916
Db	2710	 AGAGAAACTGAAACGTTTTTCAGATTTCATCTCCAATTGAAATTATAGATGAGTTCCCTACA	2769
Qy	1917	 TTTGTCAAGTTCTAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACACTGACCTAGAA	1976
Db	2770	 TTGATCAGTTCTAAAACGATTTCATTTCTAAATTAGCCAGGGAATATACTGACCTAGAA	2829
Qy	1977	 GTAGCCCACAAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTCAATTGGCTTGTGCA	2036
Db	2830	 GTATCCCACAAAAGTGAAATTGCTAATGCCCGGATGGAGCTGGGTCAATTGCCTTGACACA	2889
Qy	2037	 GGATTGCCCCATGACCTTTCTTTCAAGAGTATACAAACCTA-----AAGAGGAAGTTCAT	2090
Db	2890	 GAATTGCCCCATGACCTTTCTTTGAAGAACATACAAACCCAAAGTTGAAGAGAAAATCAGT	2949
Qy	2091	 GTCCCAGATGAGTTCTCAAAGATAGGGGTGATGTTTCAAAGGTGCCCCGACTGCCTCCA	2150
Db	2950	 TTCTCAGATGACTTTTCTAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCA	3009
Qy	2151	 GATGTTTCTGCTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAAACCCAAAGTTCTT	2210
Db	3010	 GATGTTTCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTT	3069
Qy	2211	 GTGAAAGAAGCCGAGAGAAAACCTCTCTGATACAGAAAAAGAGCGAAGATCTCCATCT	2270

Db	3070	GTGAAAGAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCT	3129
Qy	2271	GCTATATTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGAC	2330
Db	3130	GCTATATTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGAC	3189
Qy	2331	ATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTGTTCCCTGCTGCTCTCGCTGACAGTA	2390
Db	3190	ATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTCTGCTGCTTTTCATTGACAGTA	3249
Qy	2391	TTCAGCATTGTGAGTGTAACGGCCTACATTGCCTTGCCCTGCTCTCTGTGACTATCAGC	2450
Db	3250	TTCAGCATTGTGAGCGTAACAGCCTACATTGCCTTGCCCTGCTCTCTGTGACCATCAGC	3309
Qy	2451	TTTAGGATATATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATTC	2510
Db	3310	TTTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTC	3369
Qy	2511	AGGGCATATTTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTTCAGAAGTACAGCAAT	2570
Db	3370	AGGGCATATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTTCAGAAGTACAGTAAT	3429
Qy	2571	TCTGCTCTTGGTCATGTAACTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGTTGAT	2630
Db	3430	TCTGCTCTTGGTCATGTGAACTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGAT	3489
Qy	2631	GATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCC	2690
Db	3490	GATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCC	3549
Qy	2691	TGTTTCAATGGTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCCTGTT	2750
Db	3550	TGTTTCAATGGTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCCTGTT	3609
Qy	2751	ATTTATGAACGGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTT	2810
Db	3610	ATTTATGAACGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTT	3669
Qy	2811	AAAGATGCTATGGCTAAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGA	2870
Db	3670	AAAGATGCTATGGCTAAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGA	3729
Qy	2871	GAAAGCCTGAAAGAGTTAAACAATAGAGGAGTTTATCTTTAAAGGGGATATTCATTGATT	2930
Db	3730	AAACGCCCAAAATAATTA-----GTAGGAGTTCATCTTTAAAGGGGATATTCATTGATT	3784
Qy	2931	CCATTGGGGAGGGTCAGGGAAGAACAAAGCCTTGACATTGCAGTGCAGTTTCAC-----	2984
Db	3785	ATACGGGGAGGGTCAGGGAAGAACGAA-CCTTGACGTGCAGTGCAGTTTCACAGATCG	3843
Qy	2985	-----AGATCTTTATTTTATAGCAACGCAGTG-TCTGAGGAAAAATGACCTGTCTTGACTG	3038
Db	3844	TTGTTAGATCTTTATTTTATAGCCATGCACGTGTTGTGAGGAAAAATTACCTGTCTTGACTG	3903
Qy	3039	CCCTGTGTTTCATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTTAAATCGTAATCAT	3098
Db	3904	CCATGTGTTTCATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTTAAACCGTAATCAT	3963

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Qy      3099 ATTTGTTTTTCTGTATGAGGCACCTGGTGAATAAAACAAAGATCTGAGAAAGCTGTATATT 3158
          | | ||||| | ||||| | | | | | | | | | | | | | | | | | | | |
Db      3964 A--TCTTTTTCCTATCTGAGGCACCTGGTGA-----ATAAAAAACCTGTATATT 4010

Qy      3159 ACACTTTGTGCGCAGGTAGTCTTGCTGTAT-TTGGGGAATTGCAAAGAAAGTGGAGCTGAC 3217
          ||||| | | | | | | | | | | | | | | | | | | | | | | |
Db      4011 TTACTTTGTTGCAGATAGTCTTGCCGCATCTTGGCAAGTTGCAGAGATGGTGGAGCTAGA 4070

Qy      3218 AGAAATAA 3225
          | | | |
Db      4071 AAAAAAAA 4078

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RESULT 7

AAZ56886

ID AAZ56886 standard; DNA; 3579 BP.

XX

AC AAZ56886;

XX

DT 25-APR-2000 (first entry)

XX

DE Human MAGI polypeptide encoding DNA.

XX

KW MAGI protein; neuroendocrine-specific protein; neuropathy; human;
KW spinal injury; neuronal degeneration; neuromuscular disorder; cancer;
KW psychiatric disorder; developmental disorder; inflammatory disorder;
KW stroke; cytostatic; cerebroprotective; neuroprotective; ds.

XX

OS Homo sapiens.

XX

FH	Key	Location/Qualifiers
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FT	CDS	1..3579
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FT /*tag= a

```
FT                /product= "MAGI polypeptide"
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XX

PN WO200005364-A1.

XX

PD 03-FEB-2000.

XX

PF 21-JUL-1999; 99WO-GB02360.

XX

PR 22-JUL-1998; 98GB-0016024.

PR 19-JUL-1999; 99GB-0016898.

XX

PA (SMIK) SMITHKLINE BEECHAM PLC.

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PI Michalovich D, Prinjha RK;

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DR WPI; 2000-182693/16.

DR P-PSDB; AAY56967.

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PT	Novel polypeptides related to neuroendocrine-specific proteins and
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PT polynucleotides useful for diagnosis of various diseases and for

PT treatment of cancer and neurological disorders -

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PS Claim 5; Page 19-20; 35pp; English.

XX
 CC The invention relates to human MAGI protein, which is similar to
 CC neuroendocrine-specific protein. The MAGI protein can be expressed by
 CC standard recombinant methodology. The MAGI polypeptides, polynucleotides
 CC and antibodies are useful for treating diseases, including neuropathies,
 CC spinal injury, neuronal degeneration, neuromuscular disorders,
 CC psychiatric disorders and developmental disorders, cancer, stroke and
 CC inflammatory disorders. The polynucleotide is also useful for chromosome
 CC localization and for tissue expression studies. The present sequence
 CC represents a DNA encoding the human MAGI protein.
 XX
 SQ Sequence 3579 BP; 1074 A; 803 C; 812 G; 890 T; 0 other;

Query Match 58.0%; Score 2223.6; DB 21; Length 3579;
 Best Local Similarity 87.5%; Pred. No. 0;
 Matches 2519; Conservative 6000 Mis55X: 339; Indels 22; Gaps 7;

Qy	1	CTATCTCCTCTCTCAGCCGCTGCTTTTAAAGAACGTGAATACCTTGGTGATTTACCAGCA	60
Db	712	CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAATTTGTCAACA	771
Qy	61	GTA CTGCCC ACTGAAGGAACACTTCCAGCAACTTCAAATGAAGCTTCTAAAGCATTCTCA	120
Db	772	GTATTACCCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA	831
Qy	121	GAGAAGGCCAAAAATCCATTTGTAGAGAGAAATTTAACAGAAATTTTCAGAAATTGGAATAT	180
Db	832	GAGAAGGCCAAAACTCTACTCATAGATAGAGATTTAACAGAGTTTTCAGAAATTAGAATAC	891
Qy	181	TCAGAAATGGAATCATCATTCAGTGGCTCTCAAAGGCAGAACCTGCCGTAACAGTAGCG	240
Db	892	TCA DATE: GATCATCGTTCAGTGTCTCTCCAAAAGCAGAACTTGCCGTAATAGTAGCA	951
Qy	241	AATCCTAGGGACGAAATAGTTGTGAGGAGTAGAGATAAAGAAGAGGACTTAGTTAGTCTT	300
Db	952	AATCCTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGTTAGTTAGTAAT	1011
Qy	301	AACATCCTTCATACTCAGCAGGAGTTATCTACAGTCCTTACGAAATCAGTTGAAGAAGAA	360
Db	1012	AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT	1071
Qy	361	GATAGAGTTCTGTCTCCAGAAAAAACAAAGGACAGTTTTTAAGGAAAAGGGAGTTGCAGCA	420
Db	1072	GA---AGTTGTGTCTTCAGAAAAAGCAAAAGACAGTTTTTAATGAAAAGAGAGTTGCAGTG	1128
Qy	421	GAAGCTTCTATGGGGGAGGAATATGCAGACTTCAAACCATTGAGCGAGTATGGGAAGTG	480
		475	
Db	1129	GAAGCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTGAGCGAGTATGGGAAGTG	1188
Qy	481	AAAGATACTTACAAGCAAGATAGTGATGTTTTGATTGCTGGAGGTAATATAGAGAGCAAA	540
Db	1189	AAAGATAGT---AAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAAATCGAGAGCAAC	1245
Qy	541	TTGGAAGGTAAAGTGGATAAGAAACACTTTTCAGATAGCCTTGAACAAACAAATCGTGAA	600
Db	1246	TTGGAAGGTAAAGTGGATAAAAAATGTTTTGCAGATAGCCTTGAGCAAATAATCACGAA	1305

Qy 601 AAAGATAGTGAAAAGCAGTAATGATGACACTTCATTTCCCAGTACACCAGAAGCTGTAAGA 660
 |||||
 Db 1306 AAAGATAGTGAGAGTAGTAATGATGATACTTCTTTCCCAGTACGCCAGAAGGTATAAAG 1365

Qy 661 GGTGGTTCCGGAGCGTACATCACGTGTGCTCCCTTTAACC---CAACAACTGAGAATGTT 717
 |||||
 Db 1366 GATCGTCCAGGAGCATATATCACATGTGCTCCCTTTAACCAGCAGCAACTGAGAGCATT 1425

Qy 718 TCAACAAACATTTTTCCTTTGTTGGAAGATCATACTTCGGAAAAATAAGACAGATGAAAAA 777
 |||||
 Db 1426 GCAACAAACATTTTTCCTTTGTTAGGAGATCCTACTTCAGAAAAATAAGACCGATGAAAAA 1485

Qy 778 AAGATAGAA-AAAAAAGGCCACAAATTGTAACAGAGAAGAATGCAAGTGTCAAGACATCA 836
 |||||
 Db 1486 AAGATAGAA-AAAAAAGGCCACAAATTGTAACAGAGAAGAATGCAAGTGTCAAGACATCA 1545

Qy 837 AACCTTTTCCTTATGGCAGCACAGGAGTCTAAGACAGATTACGTTACAACAGATCATGTG 896
 |||||
 Db 1546 AACCTTTTCCTTATGGCAGCACAGGAGTCTAAGACAGATTACGTTACAACAGATCATGTG 1605

Qy 897 TCAAAGGTGACCGAGGAAGTAGTGGCAAACATGCCTGAAGGTCTAACCCAGATTTGGTT 956
 |||||
 Db 1606 TCAAAGGTGACCGAGGAAGTAGTGGCAAACATGCCTGAAGGTCTAACCCAGATTTGGTT 1665

Qy 957 CAGGAAGCATGTGAAAGTGAATTGAATGAAGCTACTGGTACAAAAATTGCCCTTTGAAACA 1016
 |||||
 Db 1666 CAGGAAGCATGTGAAAGTGAATTGAATGAAGCTACTGGTACAAAAATTGCCCTTTGAAACA 1725

Qy 1017 AAAATGGACCTGGTTCAAACCTTCAGAAGCTGTGCAGGAGTCACTTTACCCTGTAAACACAG 1076
 |||||
 Db 1726 AAAATGGACCTGGTTCAAACCTTCAGAAGCTGTGCAGGAGTCACTTTACCCTGTAAACACAG 1785

Qy 1077 CTTTGCCCATCTTTTGAAGAATCTGAAGCTACTCCGTACCCGTTTTCCTGACATTGTC 1136
 |||||
 Db 1786 CTTTGCCCATCTTTTGAAGAATCTGAAGCTACTCCGTACCCGTTTTCCTGACATTGTC 1845

Qy 1137 ATGGAAGCACCATTAAATTCTGTAGTTCCTAGTGCTGGTGCTTCTGCAGTGCAGCTCAGT 1196
 |||||
 Db 1846 ATGGAAGCACCATTAAATTCTGTAGTTCCTAGTGCTGGTGCTTCTGCAGTGCAGCTCAGT 1905

Qy 1197 TCATCACCATTAGAACTCTTCCTTCAGTTAATTATGAAAGCATAAAGTTTGAGCCTGAA 1256
 |||||
 Db 1906 TCATCACCATTAGAACTCTTCCTTCAGTTAATTATGAAAGCATAAAGTTTGAGCCTGAA 1962

Qy 1257 AATCCCCCACCATATGAGGAGGCCATGAATGTATCACTAAAAAAGAATCAGGAATGAAT 1316
 |||||
 Db 1963 AATCCCCCACCATATGAGGAGGCCATGAATGTATCACTAAAAAAGAATCAGGAATGAAT 2022

Qy 1317 GAAGAAATCACAGAGCCTGAAGGTATTAGTGTAGCTGTTTCAAGAAACAGAAGCTCCTTAT 1376
 |||||
 Db 2023 GAAGAAATCACAGAGCCTGAAGGTATTAGTGTAGCTGTTTCAAGAAACAGAAGCTCCTTAT 2082

Qy 1377 ATATCTATTGCATGTGATTTAATTAAAGAAACAAAGATCTCTACTGAACCGACTCCAGAT 1436
 |||||
 Db 2083 ATATCTATTGCATGTGATTTAATTAAAGAAACAAAGATCTCTACTGAACCGACTCCAGAT 2142

Qy 1437 TTCTCTAGTTATTTCAGAAATAGCAGAAGTTGCACAGCCAGTGCCCAGCATTCTGAGCTA 1496

Db	2143	TTCTCTGATTATTTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCTA	2202
Qy	1497	GTTGAAGATTCTCTCCCCGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCC	1556
Db	2203	GTTGAAGATTCTCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCT	2262
Qy	1557	GAAGTTCCACAAAAACAAGATGAAGCTGTAATACTTGTGAAAGAAAACTCACTGAAATT	1616
Db	2263	GACGTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAAGTCTCACTGAGACT	2322
Qy	1617	TCATCTGAGTCAATGACAGGACATGACAATAAGGGAAAACTCAGTGCTTCACCATCACCT	1676
Db	2323	TCATTTGAGTCAATGATAGAATATGAAAATAAGGAAAAACTCAGTGCTTTGC---CACCT	2379
Qy	1650	GAGGGGAGGAAAAACCGTATTTGGAGTCTTTTCAGCCCAGTTTAGGCATCACAAAAGATACC	1736
Db	2380	GAGGGGAGGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACC	2439
Qy	1737	TTAGCACCTGATGAAGTTTCAGCATTGACCCAAAAGGAGAAAAATCCCTTTGCAGATGGAG	1796
Db	2440	CTGTTACCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAAATCCTTTGCAGATGGAG	2499
Qy	1797	GAGCTCAATACTGCAGTTTATTCAAGTGATGGCTTATTTCATTGCTCAGGAAGCAAACCTA	1856
Db	2500	GAGCTCAGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATA	2559
Qy	1857	AGAGAAAGTGAAACATTTTCAGATTTCATCTCCGATTGAGATTATAGATGAGTTCCCGACC	1916
Db	2560	AGAGAAAGTGAAACATTTTCAGATTTCATCTCCAATTGAAATTATAGATGACTACA	2619
Qy	1917	TTTGTCTAGTTCTAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACACTGACCTAGAA	1976
Db	2620	TTGATCAGTTCTAAAACTGATTCATTTTCTAAATTAGCCAGGGAATATACTGACCTAGAA	2679
Qy	1977	GTAGCCACAAAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTTCATTGGCTTGTGCA	2036
Db	2680	GTATCCACAAAAAGTGAAATTGCTAATGCCCGGATGGAGCTGGGTTCATTGCCTTGACAA	2739
Qy	2037	GGATTGCCCCATGACCTTTCTTTCAAGAGTATACAACC-----TAAAGAGGAAGTTCAT	2090
Db	2740	GAATTGCCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGT	2799
Qy	2091	GTCCCAGATGAGTTCTCCAAAGATAGGGGTGATGTTTCAAAGGTGCCCGTACTGCCTCCA	2150
Db	2800	TTCTCAGATGACTTTTCT AAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCA	2859
Qy	2151	GATGTTTCTGCTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAAACCCAAAGTTCTT	2210
Db	2860	GATGTTTCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTT	2919
Qy	2211	GTGAAAGAAGCCGAGAGAAAACTTCCTTCTGATACAGAAAAAGAGCGAAGATCTCCATCT	2270
Db	2920	GTGAAAGAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCT	2979
Qy	2271	GCTATATTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGAC	2330

Db	2980	GCTATATTTTCAGCAGAGCTGAGTAAACTTCAGTTGTTGACCTCCTGTA	3039
Qy	2331	ATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTGTTCCCTGCTGCTCTCGCTGACAGTA	2390
Db	3040	ATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTCCTGCTGCTTTCATTGACAGTA	3099
Qy	2391	TTCAGCATTGTGAGTGTAACGGCCTACATTGCCCTTGGCCCTGCTCTCTGTGACTATCAGC	2450
Db	3100	TTCAGCATTGTGAGCGTAACAGCCTACATTGCCCTTGGCCCTGCTCTCTGTGACCATCAGC	3159
Qy	2451	TTTAGGATATATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATTC	2510
Db	3160	TTTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTC	3219
Qy	2511	AGGGCATATTTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGCAAT	2570
Db	3220	AGGGCATATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAAT	3279
Qy	2571	TCTGCTCTTGGTCATGTAACTGCACAATAAAAGAACTCAGACGCCCTCTTCTTAGTTGAT	2630
Db	3280	TCTGCTCTTGGTCATGTGAAGTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGAT	3339
Qy	2631	GATTTAGTTGATTCTCTGAAGTTTGCAGTGTGATGTGGGTATTTACCTATGTTGGTGCC	2690
Db	3340	GATTTAGTTGATTCTCTGAAGTTTGCAGTGTGATGTGGGTATTTACCTATGTTGGTGCC	3399
Qy	2691	TTGTTCAATGGTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCCTGTT	2750
Db	3400	TTGTTTAAATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCTGTT	3459
Qy	2751	ATTTATGAACGGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAAATGTT	2810
Db	3460	ATTTATGAACGGCATCAGGCGCAGATAGATCATTATCTAGGACTTGCAAATAAGAAATGTT	3519
Qy	2811	AAAGATGCTATGGCTAAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGA	2870
Db	3520	AAAGATGCTATGGCTAAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGA	3579

RESULT 8

AAF90324

ID AAF90324 standard; cDNA; 3579 BP.

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AC AAF90324;

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DT 23-JUL-2001 (first entry)

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DE Human NOGO-A cDNA.

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KW NOGO-A; human; chromosome 2p21; neuropathy; spinal injury;
 KW brain injury; stroke; neuronal degeneration; Alzheimer's disease;
 KW Parkinson's disease; neuromuscular disorder; psychiatric disorder;
 KW developmental disorder; neuroprotective; nootropic; neuroleptic;
 KW antiparkinsonian; cerebroprotective; neuroleptic; diagnosis;
 KW therapy; ss.

XX

OS Homo sapiens.

Qy	181	TCAGAAATGGAATCATCATTAGTGGCTCTCAAAAGGCAGAACCTGCCGTAACAGTAGCG	240
Db	892	TCAGAAATGGGATCATCGTTAGTGTCTCTCCAAAAGCAGAATCTGCCGTAATAGTAGCA	951
Qy	241	AATCCTAGGGACGAAATAGTTGTGAGGAGTAGAGATAAAGAAGAGGACTTAGTTAGTCTT	300
Db	952	AATCCTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGTTAGTTAGTAAT	1011
Qy	301	AACATCCTTCATACTCAGCAGGAGTTATCTACAGTCCTTACGAAATCAGTTGAAGAAGAA	360
Db	1012	AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT	1071
Qy	361	GATAGAGTTCTGTCTCCAGAAAAACAAAGGACAGTTTTTAAGGAAAAGGGAGTTGCAGCA	420
Db	1072	GA--AGTTGTGTCTTCAGAAAAAGCAAAGACAGTTTTTAATGAAAAGAGAGTTGCAGTG	1128
Qy	421	GAAGCTTCTATGGGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG	480
Db	1129	GAAGCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG	1188
Qy	481	AAAGATACTTACAAGCAAGATAGTGATGTTTTGATTGCTGGAGGTAATATAGAGAGCAAA	540
Db	1189	AAAGATAGT--AAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAAATCGAGAGCAAC	1245
Qy	541	TTGGAAGGTAAAGTGGATAAGAAACACTTTTTTCAGATAGCCTTGAAACAAACAAATCGTGAA	600
Db	1246	TTGGAAGGTAAAGTGGATAAAAAATGTTTTGCAGATAGCCTTGAGCAAATAATCACGAA	1305
Qy	601	AAAGATAGTGAAAGCAGTAATGATGACACTTCATTTCCCAGTACACCAGAAGCTGTAAGA	660
Db	1306	AAAGATAGTGAGAGTAGTAATGATGATACTTCTTTCCCCAGTACGCCAGAAGGTATAAAG	1365
Qy	661	GGTGGTTCCGGAGCGTACATCACGTGTGCTCCCTTTAACC--CAACAAGTGAATGTT	717
Db	1366	GATCGTCCAGGAGCATATATCACATGTGCTCCCTTTAACCCAGCAGCAACTGAGAGCATT	1425
Qy	718	TCAACAAACATTTTTCCCTTGTTGGAAGATCATACTTCGGAAAATAAGACAGATGAAAAA	777
Db	1426	GCAACAAACATTTTTCTTTGTTAGGAGATCCTACTTCAGAAAATAAGACCGATGAAAAA	1485
Qy	778	AAGATAGAA-AAAAAAGGCACAAATTGTAACAGAGAAGAATGCAAGTGTAAGACATCA	836
Db	1486	AAAATAGAAGAAAAGAAGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAAACATCA	1545
Qy	837	AACCCTTTCTTTATGGCAGCACAGGAGTCTAAGACAGATTACGTTACAACAGATCATGTG	896
Db	1546	AACCCTTTCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATTTA	1605
Qy	897	TCAAAGGTGACCGAGGAAGTAGTGGCAAACATGCCTGAAGGTCTAACCCAGATTTGGTT	956
Db	1606	ACAAAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTA	1665
Qy	957	CAGGAAGCATGTGAAAGTGAATTGAATGAAGCTACTGGTACAAAAATTGCCTTTGAAACA	1016
Db	1666	CAGGAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACA	1725

Qy	1017	AAAATGGACCTGGTTCAAACCTTCAGAAGCTGTGCAGGAGTCACTTTACCCTGTAACACAG	1076
Db	1726	AAAATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAG	1785
Qy	1077	CTTTGCCCATCTTTTGAAGAATCTGAAGCTACTCCGTCACCGGTTTTGCCTGACATTGTC	1136
Db	1786	CTTTGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGCCTGACATTGTT	1845
Qy	1137	ATGGAAGCACCATTAAATTCTGTAGTTCCTAGTGCTGGTGCTTCTGCAGTGCAGCTCAGT	1196
Db	1846	ATGGAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCAGC	1905
Qy	1197	TCATCACCATTAGAACTCTTCCTTCAGTTAATTATGAAAGCATAAAGTTTTGAGCCTGAA	1256
Db	1906	TC TAGAAGC --- TCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAA	1962
Qy	1257	AATCCCCCACCATATGAGGAGGCCATGAATGTATCACTAAAAAAGAATCAGGAATGAAT	1316
Db	1963	AACCCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAG	2022
Qy	1317	GAAGAAATCACAGAGCCTGAAGGTATTAGTGTAGCTGTTTCAGGAAACAGAAGCTCCTTAT	1376
Db	2023	GAAGAAATTAAAGAGCCTGAAAAATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTAT	2082
Qy	1377	ATATCTATTGCATGTGATTTAATTAAAGAAACAAAGATCTCTACTGAACCGACTCCAGAT	1436
Db	2083	ATATCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCAGCTCCGGAT	2142
Qy	1437	TTCTCTAGTTATTTCAGAAATAGCAGAAGTTGCACAGCCAGTGCCCCGAGCATTCTGAGCTA	1496
Db	2143	TTCTCTGATTATTTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCTA	2202
Qy	1497	GTTGAAGATTCTCCCCCGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCC	1556
Db	2203	GTTGAAGATTCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCT	2262
Qy	1557	GAAGTTCCACAAAAACAAGATGAAGCTGTAATACTTGTGAAAGAAAACCTCACTGAAATT	1616
Db	2263	GACGTTCCACAAAAACAAGATGAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACT	2322
Qy	1617	TCATCTGAGTCAATGACAGGACATGACAATAAGGGAAAACTCAGTGCTTCACCATCACCT	1676
Db	2323	TCATTTGAGTCAATGATAGAATATGAAAAATAAGGAAAAACTCAGTGCTTTGC---CACCT	2379
Qy	1677	GAGGGAGGAAAACCGTATTTGGAGTCTTTTCAGCCAGTTTAGGCATCACAAAAGATACC	1736
Db	2380	GAGGGAGGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACC	2439
Qy	1737	TTAGCACCTGATGAAGTTTCAGCATTGACCCAAAAGGAGAAAATCCCTTTGCAGATGGAG	1796
Db	2440	CTGTTACCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAATTCCTTTGCAGATGGAG	2499
Qy	1797	GAGCTCAATACTGCAGTTTATTCAAGTGATGGCTTATTCATTGCTCAGGAAGCAAACCTA	1856
Db	2500	GAGCTCAGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATA	2559
Qy	1857	AGAGAAAGTGAAACATTTTCAGATTTCATCTCCGATTGAGATTATAGATGAGTTCCCGACC	1916

Db	2560	AGAGAAACTGAAACGTTTTCAGATTTCATCTCCAATTGAAATTATAGATGAGTTCCTTACA	2619
Qy	1917	TTTGTTCAGTTCTAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACACTGACCTAGAA	1976
Db	2620	TTGATCAGTTCTAAAACTGATTCAATTTCTAAATTAGCCAGGGAATATACTGACCTAGAA	2679
Qy	1977	GTAGCCCACAAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTTCATTGGCTTGTGCA	2036
Db	2680	GTATCCCACAAAAGTGAAATTGCTAATGCCCGGATGGAGCTGGGTTCATTGCCTTGACA	2739
Qy	2037	GGATTGCCCCATGACCTTTCTTTCAAGAGTATACAACC-----TAAAGAGGAAGTTCAT	2090
Db	2740	GAATTGCCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGT	2799
Qy	209	AAAGATAGGGGTGATGTTTCAAAGGTGCCCGTACTGCCTCCA	2150
Db	2800	TTCTCAGATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCA	2859
Qy	2151	GATGTTTCTGCTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAAACCCAAAGTTCTT	2210
Db	2860	GATGTTTCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTT	2919
Qy	2211	GTGAAAGAAGCCGAGAGAAAACTTCCTTCTGATACAGAAAAAGAGCGAAGATCTCCATCT	2270
Db	2920	GTGAAAGAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCT	2979
Qy	TITLE 0271	GCTATATTTTAACTCGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGAC	2330
Db	2980	GCTATATTTTAACTCGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTGTACTG*pGAGAC	3039
Qy	2331	ATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTGTTCTGCTGCTCTCGCTGACAGTA	2390
Db	3040	ATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTCTGCTGCTTTTCATTGACAGTA	3099
Qy	2391	TTCAGCATTGTGAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCTGTGACTATCAGC	2450
Db	3100	TTCAGCATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGC	3159
Qy	2451	TTTAGGATATATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATTC	2510
Db	3160	TTTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTC	3219
Qy	2511	AGGGCATATTTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTTCAGAAGTACAGCAAT	2570
Db	3220	AGGGCATATCTGGAATCTGAAGT 50XT GAGGAGTTGGTTTCAGAAGTACAGTAT	3039
Qy	2571	TCTGCTCTTGGTCATGTTAACTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGTTGAT	2630
Db	3280	TCTGCTCTTGGTCATGTGAACGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGAT	3339
Qy	2631	GATTTAGTTGATTCTCTGAAGTTTGAGTGTGGGTATTTACCTATGTTGGTGCC	2690
Db	3340	GATTTAGTTGATTCTCTGAAGTTTGAGTGTGGGTATTTACCTATGTTGGTGCC	3399
Qy	2691	TTGTTCAATGGTCTGACACTACTAATTTGGCTCTGATTTCACTCTTCAGTGTTCCTGTT	2750

Db 3400 TTGTTTAAATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCCTGTT 3459

Qy 2751 ATTTATGAACGGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTT 2810
 |||

Db 3460 ATTTATGAACGGCATCAGGCGCAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTT 3519

Qy 2811 AAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGA 2870
 |||

Db 3520 AAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGAATGA 3579

RESULT 9

ABN86601

ID ABN86601 standard; DNA; 3579 BP.

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AC ABN86601;

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DT 05-NOV-2002 (first entry)

XX

DE Human neurotransmitter receptor protein Nogo encoding DNA.

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KW Nerve regeneration; neuroprotection; neuronal degeneration; CNS; PNS;
 KW central nervous system; peripheral nervous system; tranquillizer; Nogo;
 KW vulnerary; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant;
 KW nootropic; antiparkinsonian; ophthalmological; analgesic; hepatotropic;
 KW osteopathic; vasotropic; nephrotropic; cytostatic; antigen; gene therapy;
 KW neurotransmitter receptor; human; gene; ds.

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OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 1..3579

FT /*tag= a

FT /product= "Nogo"

FT /note= "Nogo-A, Nogo-B and Nogo-C"

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PN US2002072493-A1.

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PD 13-JUN-2002.

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PF 28-JUN-2001; 2001US-0893348.

XX

PR 19-MAY-1998; 98IL-0124500.

PR 21-JUL-1998; 98WO-US14715.

PR 22-DEC-1998; 98US-0218277.

PR 19-MAY-1999; 99US-0314161.

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PA (YEDA) YEDA RES & DEV CO LTD.

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PI Eisenbach-Schwartz M, Hauben E, Cohen IR, Beserman P, Mosonego A;
 PI Moalem G;

XX

DR WPI; 2002-607255/65.

DR P-PSDB; ABB81078, ABB81079, ABB81080.

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PT Promoting nerve regeneration and preventing neuronal degeneration in
 PT the central/peripheral nervous system from injury/disease, comprises

PT administering nervous system-specific activated T cells/antigen, or
PT analogs/peptides -
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PS Disclosure; Page 49-53; 93pp; English.
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CC The invention relates to promoting nerve regeneration or conferring
CC neuroprotection and preventing or inhibiting neuronal degeneration in the
CC central/peripheral nervous system (NS). The method involves administering
CC NS-specific activated T cells, NS-specific antigen, its analogue or its
CC peptide, a nucleotide sequence the NS-specific antigen or its analogue or
CC combinations. The method is useful for promoting nerve regeneration and
CC preventing neuronal degeneration in central/peripheral nervous system
CC from injury/disease, where the injury is spinal cord injury, blunt
CC trauma, penetrating trauma, hemorrhagic stroke, ischaemic stroke or
CC damages caused by surgery such as tumour excision. The disease is not an
CC autoimmune disease or neoplasm. The disease results in a degenerative
CC process occurring in either gray or white matter or both. The disease
CC is diabetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's
CC disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea,
CC amyotrophic lateral sclerosis, non-arteritic optic neuropathy, and
CC vitamin deficiency, intervertebral disc herniation, prion diseases such
CC as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral
CC neuropathies associated with various diseases, including but not limited
CC to uremia, porphyria, hypoglycemia, Sjorgren Larsson syndrome, acute
CC sensory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary
CC amyloidosis, obstructive lung diseases, acromegaly, malabsorption
CC syndromes, polycythemia vera, immunoglobulin - and IgG gamma-
CC pathies, complications of various drugs (e.g., metronidazole) and toxins
CC (e.g. alcohol, barbiturates, organophosphates) No Charcot-Marie-Tooth disease, ataxia
CC telangiectasia, Friedreich's ataxia, amyloid polyneuropathies,
CC adrenomyeloneuropathy, Fabry's disease, or lipoproteinemia. The present sequence represents a DNA
CC encoding the human neurotransmitter receptor protein Nogo (Nogo-A, Nogo-B
CC and Nogo-C), an example of NS-specific antigen.
XX
SQ Sequence 3579 BP; 1074 A; 803 C; 812 G; 890 T; 0 other;

Query Match 58.0%; Score 2223.6; DB 24; Length 3579;
Matches 2519; Conservative 0; Mismatches 339; Indels 22; Gaps 7;

Qy	1	CTATCTCCTCTCTCAGCCGCTGCTTTTAAAGAACGTGAATACCTTGGTGATTACAGCA	60
Db	712	CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAATTTGTCAACA	771
Qy	61	GTAAGGCAAAATCCATTTGTAGAGAGAAATTTAACAGAAATTTTCAGAAATGGAATAT	120
Db	772	GTATTACCCACTGAAGGAACACTTCAAGAAAATGTAGTGAAGCTTCTAAAGAGGTCTCA	831
Qy	121	GAGAAGGCAAAATCCATTTGTAGAGAGAAATTTAACAGAAATTTTCAGAAATGGAATAT	180
Db	832	GAGAAGGCAAAATCTACTCATAGATAGAGATTTAACAGAGTTTTCAGAAATGGAATAT	891
Qy	181	TCAGAAATGGAATCATCATTAGTGGCTCTCAAAGGCAGAACCTGCCGTAAAGTAGCG	240
Db	892	TCAGAAATGGGATCATCGTTAGTGTCTCTCAAAGGCAGAAATCTGCCGTAAAGTAGCA	951

Qy	241	AATCCTAGGGACGAAATAGTTGTGAGGAGTAGAGATAAAGAAGAGGACTTAGTTAGTCTT	300
Db	952		
		AATCCTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGTTAGTTAGTAAT	1011
Qy	301	AACATCCTTCATACTCAGCAGGAGTTATCTACAGTCCTTACGAAATCAGTTGAAGAAGAA	360
Db	1012		
		AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT	1071
Qy	361	GATAGAGTTCTGTCTCCAGAAAAACAAAGGACAGTTTTTAAGGAAAAGGGAGTTGCAGCA	420
Db	1072	GA---AGTTGTGTCTTCAGAAAAAGCAAAGACAGTTTTTAATGAAAAGAGAGTTGCAGTG	1128
Qy	421	GAAGCTTCTATGGGGGAGGAATATGCAGACTTCAAACCATTGTAGCGAGTATGGGAAGTG	480
Db	1129		
		GAAGCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTGTAGCGAGTATGGGAAGTG	1188
Qy	481	AAAGATACTTACAAGCAAGATAGTGATGTTTTTGATTGCTGGAGGTAATATAGAGAGCAAA	540
Db	1189		
		AAAGATAGT---AAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAAATCGAGAGCAAC	1245
Qy	541	TTGGAAGGTAAAGTGGATAAGAAACACTTTTCAGATAGCCTTGAACAAACAAATCGTGAA	600
Db	1246		
		TTGGAAGGTAAAGTGGATAAAAAATGTTTTGCAGATAGCCTTGAGCAAACCTAATCACGAA	1305
Qy	601	AAAGATAGTGAAAGCAGTAATGATGACACTTCATTTCCCAGTACACCAGAAGCTGTAAGA	660
Db	1306		
		AAAGATAGTGAGAGTAGTAATGATGATACTTCTTTCCCCAGTACGCCAGAAGGTATAAAG	1365
Qy	661	GGTGGTTCCGGAGCGTACATCACGTGTGCTCCCTTTAACC---CAACAAC TGAGAATGTT	717
Db	1366		
		GATCGTCCAGGAGCATATATCACATGTGCTCCCTTTAACCAGCAGCAACTGAGAGCATT	1425
Qy	718	TCAACAAACATTTTTCCCTTGTTGGAAGATCATACTTCGGAATAAAGACAGATGAAAAA	777
Db	1426		
		GCAACAAACATTTTTCTTTGTTAGGAGATCCTACTTCAGAAAATAAGACCGATGAAAAA	1485
Qy	778	AAGATAGAA-AAAAAAGGCACAAATTGTAACAGAGAAGAATGCAAGTGTCAAGACATCA	836
Db	1486		
		AAAATAGAAGAAAAGAAGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAAACATCA	1545
Qy	837	AACCCTTTCTTTATGGCAGCACAGGAGTCTAAGACAGATTACGTTACAACAGATCATGTG	896
Db	1546		
		AACCCTTTCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCAACAGATAATTTA	1605
Qy	897	TCAAAGGTGACCGAGGAAGTAGTGGCAAACATGCCTGAAGGTCTAACCCAGATTGGTT	956
Db	1606		
		ACAAAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTAGTA	1665
Qy	957	CAGGAAGCATGTGAAAGTGAATTGAATGAAGCTACTGGTACAAAAATTGCCTTTGAAACA	1016
Db	1666		
		CAGGAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACA	1725
Qy	1017	AAAATGGACCTGGTTCAAACCTCAGAAGCTGTGCAGGAGTCACTTTACCCTGTAACACAG	1076
Db	1726		
		AAAATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAG	1785
Qy	1077	CTTTGCCCATCTTTTGAAGAATCTGAAGCTACTCCGTCACCGGTTTTGCCTGACATTGTC	1133

Db	1786	 CTTTGCCCATCATTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTGCCTGACATTGTT	1845
Qy	1137	ATGGAAGCACCATTAAATTCTGTAGTTCCTAGTGCTGGTGCTTCTGCAGTGCAGCTCAGT	1196
Db	1846	 ATGGAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCAGC	1905
Qy	1197	TCATCACCATTAGAAACTCTTCCTTCAGTTAATTATGAAAGCATAAAGTTTGAGCCTGAA	1256
Db	1906	 TCATCACCATTAGAAAGC---TTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAA	1962
Qy	1257	AATCCCCCACCATATGAGGAGGCCATGAATGTATCACTAAAAAAGAATCAGGAATGAAT	1316
Db	1963	 AATCCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAG	2022
Qy	1300	GAAGAAATCACAGAGCCTGAAGGTATTAGTGTAGCTGTTTCAGGAAACAGAAGCTCCTTAT	1376
Db	2023	 GAAGAAATTAAGAGCCTGAAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTAT	2082
Qy	1377	ATATCTATTGCATGTGATTAAATTAAAGAAACAAAGATCTCTACTGAACCGACTCCAGAT	1436
Db	2083	 ATATCTATTGCATGTGATTAAATTAAAGAAACAAAGCTTTCTGCTGAACCGACTCCGGAT	2142
Qy	1437	TTCTCTAGTTATTTCAGAAATAGCAGAAGTTGCACAGCCAGTGCCCGAGCATTCTGAGCTA	1496
Db	2143	 TTCTCTGATTATTTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCTA	2202
Qy	1497	GTTGAAGATTCCCTCCCCGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCC	1556
Db	2203	 GTTGAAGATTCCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCT	2262
Qy	1557	GAAGTTCACAAAAACAAGATGAAGCTGTAATACTTGTGAAAGAAAACCTCACTGAAATT	1616
Db	2263	 GACGTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACT	2322
Qy	1617	TCATCTGAGTCAATGACAGGACATGACAATAAGGGAAAACTCAGTGCTTCACCATCACCT	1676
Db	2323	 TCATTTGAGTCAATGATAGAAATATGAAAATAAGGAAAACTCAGTGCTTTGC---CACCT	2379
Qy	1677	GAGGGAGGAAAACCGTATTTGGAGTCTTTTCAGCCCAGTTTAGGCATCACAAAAGATACC	1736
Db	2380	 GAGGGAGGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACC	2439
Qy	1737	TTAGCACCTGATGAAGTTTCAGCATTGACCCAAAAGGAGAAAAATCCCTTTGCAGATGGAG	1796
Db	2440	 CTGTTACCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAATTCCTTTGCAGATGGAG	2499
Qy	1797	GAGCTCAATACTGCAGTTTATTCAAGTGATGGCTTATTCATTGCTCAGGAAGCAAACCTA	1856
Db	2500	 GAGCTCAGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATA	2559
Qy	1857	AGAGAAAGTGAAACATTTTCAGATTCACTCCGATTGAGATTATAGATGAGTTCCCGACC	1916
Db	2560	 AGAGAAACTGAAACGTTTTCAGATTCACTCCAATTGAAATTATAGATGAGTTCCCTACA	2619
Qy	1917	TTTGTCAAGTTCTAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACACTGACCTAGAA	1976

Db	2620	TTGATCAGTTCTTAAAACTGATTTCATTTTCTAAATTAGCCAGGGAATATACTGACCTAGAA	2679
Qy	1977	GTAGCCCACAAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTTCATTGGCTTGTGCA	2036
Db	2680	GTATCCCACAAAAGTGAAATTGCTAATGCCCCGGATGGAGCTGGGTTCATTGCCTTGCACA	2739
Qy	2037	GGATTGCCCATGACCTTTCTTTCAAGAGTATACAACC-----TAAAGAGGAAGTTCAT	2090
Db	2740	GAATTGCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGT	2799
Qy	2091	GTCCCAGATGAGTTCTCCAAAGATAGGGGTGATGTTTCAAAGGTGCCCGTACTGCCTCCA	2150
Db	2800	TTCTCAGATGACTTTTCTAAAAATGGGTCTGTACATCAAAGGTGCTCTTATTGCCTCCA	2859
Qy	2151	GATGTTTCTGCTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAAACCCAAAGTTCTT	2210
Db	2860	GATGTTTCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTT	2919
Qy	2211	GTGAAAGAAGCCGAGAGAAAACTTCCTTCTGATACAGAAAAAGAGCGAAGATCTCCATCT	2270
Db	2920	GTGAAAGAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCT	2979
Qy	2271	GCTATATTTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGAC	2330
Db	2980	GCTATATTTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGAC	3039
Qy	2331	ATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTGTTCTCTGCTGCTCTCGCTGACAGTA	2390
Db	3040	ATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTATTCCTGCTGCTTTTCATTGACAGTA	3099
Qy	2391	TTCAGCATTGTGAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCTGTGACTATCAGC	2450
Db	3100	TTCAGCATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGC	3159
Qy	2451	TTTAGGATATATAAGGGTGTGATCCAGGCATCCAGAAATCTGATGAAGGCCACCCATTTC	2510
Db	3160	TTTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTTC	3219
Qy	2511	AGGGCATATTTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTTCTGAGTACAGCAAT	2570
Db	3220	AGGGCATATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTTCTGAGTACAGTAAT	3279
Qy	2571	TCTGCTCTTGGTCATGTAACTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGTTGAT	2630
Db	3280	TCTGCTCTTGGTCATGTGAACTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGAT	3339
Qy	2631	GATTTAGTTGATTCTCTGAAGTTTGAGTGTGATGTGGGTATTTACCTATGTTGGTGCC	2690
Db	3340	GATTTAGTTGATTCTCTGAAGTTTGAGTGTGATGTGGGTATTTACCTATGTTGGTGCC	3399
Qy	2691	TTGTTCAATGGTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCCTGTT	2750
Db	3400	TTGTTTAAATGGTCTGACACTACTGATTTTGGCTCTCATTTCACCTCTTCAGTGTTCCTGTT	3459
Qy	2751	ATTTATGAACGGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTT	2810
Db	3460	ATTTATGAACGGCATCAGGCGCAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTT	3519

Qy 2811 AAAGATGCTATGGCTAAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGA 2870
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 3520 AAAGATGCTATGGCTAAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGAATGA 3579

RESULT 10

ABK90134

ID ABK90134 standard; DNA; 3579 BP.

XX

AC ABK90134;

XX

DT 21-OCT-2002 (first entry)

XX

DE DNA encoding human NogoA protein.

XX

KW Human; Nogo; BACE; acute neuronal injury; spinal injury; head injury;
 KW stroke; peripheral nerve damage; neoplastic disorder; glioblastoma;
 KW neuroblastoma; hyperproliferative disorder; dysproliferative disorder;
 KW cirrhosis; psoriasis; keloid formation; fibrocystic condition; cancer;
 KW tissue hypertrophy; central nervous system; axon regeneration; NogoA;
 KW Nogo-associated disease; metastasis; gene; ds.

XX

OS Homo sapiens.

XX

FH Key 50X| Location/Qualifiers |||

FT CDS 1..3579

FT /*tag= a

FT /product= "Human NogoA protein"

XX

PN WO200257483-A2.

XX

PD 25-JUL-2002.

XX

PF 18-JAN-2002; 2002WO-GB00228.

XX

PR 18-JAN-2001; 2001GB-0001312.

XX

PA (GLAX) GLAXO GROUP LTD.

PA (SMIK) SMITHKLINE BEECHAM PLC.

XX

PI Blackstock WP, Hale RS, Prinjha R, Rowley A;

XX

DR WPI; 2002-599722/64.

DR P-PSDB; ABG30938.

XX

PT Identifying modulators of Nogo or BACE activity for treating acute
 PT neuronal injuries, neoplastic or dysproliferative disorders, comprises
 PT providing and monitoring interaction between Nogo and BACE polypeptides

PT -

XX

PS Disclosure; Page 53-58; 68pp; English.

XX

CC The present invention relates to a new method of identifying modulators
 CC of Nogo function or BACE activity. The method involves providing Nogo and
 CC BACE polypeptides capable of binding with each other, monitoring the
 CC interaction between these polypeptides, and determining if the test agent

Qy	481	AAAGATACTTACAAGCAAGATAGTGATGTTTTCAGATTGCTGGAGGTAATATAGAGAGCAAA	540
Db	1189	AAAGATAGT---AAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAATAATCGAGAGCAAC	1245
Qy	541	TTGGAAGGTAAAGTGGATAAGAAACACTTTTTCAGATAGCCTTGAACAAAACAAATCGTGAA	600
Db	1246	TTGGAAGGTAAAGTGGATAAAAAATGTTTTGCAGATAGCCTTGAGCAAACATAATCACGAA	1305
Qy	601	AAAGATAGTGAAAGCAGTAATGATGACACTTCATTTCCCAGTACACCAGAAGCTGTAAGA	660
Db	1306	AAAGATAGTGAGAGTAGTAATGATGATACTTCTTTCCCAGTACGCCAGAAGGTATAAAG	1365
Qy	661	GGTGGTTCCGGAGCGTACATCACGTGTGCTCCCTTTAACC---CAACAACAGAGAATGTT	717
Db	1366	GATCGTCCAGGAGCATATATCATGTGCTCCCTTTAACCAGCAGCAACTGAGAGCATT	1425
Qy	718	TCAACAAAACATTTTTCCCTTGTTGGAAGATCATACTTCGGAAAAATAAGACAGATGAAAAA	777
Db	1426	GCAACAAAACATTTTTCCCTTGTTAGGAGATCCTACTTCAGAAAAATAAGACCGATGAAAAA	1485
Qy	778	AAGATAGAA-AAAAAAGGCACAAATTGTAACAGAGAAGAAATGCAAGTGTCAAGACATCA	836
Db	1486	AAAATAGAAAGAAAAGAAGGCCAAATAGTAACAGAGAAGAAATACTAGCACCAAAACATCA	1545
Qy	837	AACCCTTTCTTATGGCAGCACAGGAGTCTAAGACAGATTACGTTACAACAGATCATGTG	896
Db	1546	AACCCTTTCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATTTA	1605
Qy	897	TCAAAGGTGACCGAGGAAGTAGTGGCAAACATGCCTGAAGGTCTAACCCAGATTTGGTT	956
Db	1606	ACAAAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCTGACTCCAGATTTAGTA	1665
Qy	957	CAGGAAGCATGTGAAAGTGAATTGAATGAAGCTACTGGTACAAAAATTGCCTTTGAAACA	1016
Db	1666	CAGGAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACA	1725
Qy	1017	AAAATGGACCTGGTTCAAACCTTCAGAAGCTGTGCAGGAGTCACTTTACCCTGTAACACAG	1076
Db	1726	AAAATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAG	1785
Qy	1077	CTTTGCCCATCTTTTGAAGAATCTGAAGCTACTCCGTCACCGTTTTGCCTGACATTGTC	1136
Db	1786	CTTTGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTGCCTGACATTGTT	1845
Qy	1137	ATGGAAGCACCATTAATAATTCTGTAGTTCCTAGTGCTGGTGCTTCTGCAGTGCAGCTCAGT	1196
Db	1846	ATGGAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCAGC	1905
Qy	1197	TCATCACCATTAGAAACTCTTCCTTCAGTTAATTATGAAAGCATAAAGTTTGAGCCTGAA	1256
Db	1906	TCATCACCATTAGAAAGC---TTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAA	1962
Qy	1257	AATCCCCCACCATATGAGGAGGCCATGAATGTATCACTAAAAAAGAATCAGGAATGAAT	1316
Db	1963	AATCCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAG	2022
Qy	1317	GAAGAAATCACAGAGCCTGAAGGTATTAGTGTAGCTGTTTCAGGAAACAGAAGCTCCTTAT	1376

Db	2023	GAAGAAATTAAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTAT	2082
Qy	1377	ATATCTATTGCATGTGATTTAATTAAAGAAACAAAGATCTCTACTGAACCGACTCCAGAT	1436
Db	2083	ATATCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCGACTCCGGAT	2142
Qy	1437	TTCTCTAGTTATTTCAGAAATAGCAGAAGTTGCACAGCCAGTGCCCCGAGCATTCTGAGCTA	1496
Db	2143	TTCTCTGATTATTTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCTA	2202
Qy	1497	GTTGAAGATTCCCTCCCCGATTCTGAACCGATTGACTTATTTAGTGATGATTCAATACCC	1556
Db	2203	GTTGAAGATTCCCTCACCTGATTCTGAACCGATTGACTTATTTAGTGATGATTCAATACCT	2262
Qy	1557	GAAGTTCCACAAAAACAAGATGAAGCTGTAATACTTGTGAAAGAAAACCTCACTGAAATT	1616
Db	2263	GACGTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACT	2322
Qy	1617	TCATCTGAGTCAATGACAGGACATGACAATAAGGGAAAACTCAGTGCTTCACCATCACCT	1676
Db	2323	TCATTTGAGTCAATGATAGAATATGAAAATAAGGAAAACTCAGTGCTTTGC---CACCT	2379
Qy	1677	GAGGGAGGAAAACCGTATTTGGAGTCTTTTCAGCCCGAGTTTAGGCATCACAAAAGATACC	1736
Db	2380	GAGGGAGGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACC	2439
Qy	1737	TTAGCACCTGATGAAGTTTCAGCATTGACCCAAAAGGAGAAAATCCCTTTGCAGATGGAG	1796
Db	2440	CTGTTACCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAATTCCTTTGCAGATGGAG	2499
Qy	1797	GAGCTCAATACTGCAGTTTATTCAAGTGATGGCTTATTCATTGCTCAGGAAGCAAACCTA	1856
Db	2500	GAGCTCAGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATA	2559
Qy	1857	AGAGAAAGTGAAACATTTTCAGATTTCATCTCCGATTGAGATTATAGATGAGTTCCCGACC	1916
Db	2560	AGAGAAACTGAAACGTTTTCAGATTTCATCTCCAATTGAAATTATAGATGAGTTCCCTACA	2619
Qy	1917	TTTGTCAAGTTCTAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACACTGACCTAGAA	1976
Db	2620	TTGATCAGTTCTAAAACTGATTTCATTTCTAAATTAGCCAGGGAATATACTGACCTAGAA	2679
Qy	1977	GTAGCCACAAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTTCATTGGCTTGTGCA	2036
Db	2680	GTATCCACAAAAGTGAAATTGCTAATGCCCCGGATGGAGCTGGGTTCATTGCCTTGCACA	2739
Qy	2037	GGATTGCCCCATGACCTTTCTTTCAAGAGTATACAACC-----TAAAGAGGAAGTTCAT	2090
Db	2740	GAATTGCCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGT	2799
Qy	2091	GTCCCGATGAGTTCTCCAAAGATAGGGGTGATGTTTCAAAGGTGCCCGTACTGCCTCCA	2150
Db	2800	TTCTCAGATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCA	2859
Qy	2151	GATGTTTCTGCTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAAACCCAAAGTTCCTT	2210

Db	2860	GATGTTTCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTT	2919
Qy	2211	GTGAAAGAAGCCGAGAGAAAACTTCCTTCTGATACAGAAAAAGAGCGAAGATCTCCATCT	2270
Db	2920	GTGAAAGAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCT	2979
Qy	2271	GCTATATTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGAC	2330
Db	2980	GCTATATTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGAC	3039
Qy	2331	ATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTGTTTCCTGCTGCTCTCGCTGACAGTA	2390
Db	3040	ATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTCTGCTGCTTTTCATTGACAGTA	3099
Qy	2391	TTCAGCATTGTGAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCTGTGACTATCAGC	2450
0XG			
Db	3100	TTCAGCATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGC	3159
Qy	2451	TTTAGGATATATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATTC	2510
Db	3160	TTTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTC	3219
Qy	2511	AGGGCATATTTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGCAAT	2570
Db	3220	AGGGCATATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAAT	3279
Qy	2571	TCTGCTCTTGGTCATGTAACTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGTTGAT	2630
Db	3280	TCTGCTCTTGGTCATGTGAACTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGAT	3339
Qy	2631	GATTTAGTTGATTCTCTGAAGTTGCACTGTTGATGTGGGTATTT	2690
Db	3340	GATTTAGTTGATTCTCTGAAGTTGCACTGTTGATGTGGGTATTTACCTATGTTGGTGCC	3399
Qy	2691	TTGTTCAATGGTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCCCTGTT	2750
Db	3400	TTGTTTAAATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCCTGTT	3459
Qy	2751	ATTTATGAACGGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTT	2810
Db	3460	ATTTATGAACGGCATCAGGCGCAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTT	3519
Qy	2811	AAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGA	2870
Db	3520	AAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGA	3579

RESULT 11

AAD01173

ID AAD01173 standard; cDNA; 4684 BP.

XX

AC AAD01173;

XX

DT 02-NOV-2000 (first entry)

XX

DE Rat neurite growth inhibitor Nogo A cDNA.

XX

KW Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;
KW central nervous system; neoplastic disease; antiproliferative; glioma;
KW antisense gene therapy; neuroblastoma; menagioma; retinoblastoma;
KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
KW structural plasticity; screening; ss.

XX

OS Rattus sp.

XX

FH Key Location/Qualifiers

FT CDS 253..3744

FT /*tag= a

FT /product= "Nogo A"

FT /transl_except= (pos:1462..1464, aa:Ile)

XX

PN WO200031235-A2.

XX

PD 02-JUN-2000.

XX

PF 05-NOV-1999; 99WO-US26160.

XX

PR 06-NOV-1998; 98US-0107446.

XX

PA (SCHW/) SCHWAB M E.

PA (CHEN/) CHEN M S.

XX

PI Schwab ME, Chen MS;

XX

DR WPI; 2000-400052/34.

DR P-PSDB; AAY71310.

XX

PT Nogo proteins and nucleic acids useful for treating neoplastic
PT disorders of the central nervous system and inducing regeneration of
PT neurons -

XX

PS Claim 26; Fig 2A; 122pp; English.

XX

CC The present sequence is a cDNA encoding rat Nogo A protein which is a
CC potent neural cell growth inhibitor and is free of all central nervous
CC system (CNS) myelin material with which it is natively associated.
CC The present sequence was generated by fusing R018U37-3, R1-3U21 cDNA
CC sequences isolated from hexanucleotides-primed rat brain stem/spinal cord
CC library, and Oli18 cDNA from an oligo d(T)-primed rat oligodendrocyte
CC library. Nogo proteins and fragments displaying neurite growth inhibitory
CC activity are used in the treatment of neoplastic disease of the CNS
CC e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma, ependyoma,
CC pinealoma, haemangioblastoma, acoustic neuroma, oligodendroglioma,
CC menagioma, neuroblastoma or retinoblastoma and degenerative nerve
CC diseases e.g. Alzheimer's and Parkinson's diseases. Therapeutics which
CC promote Nogo activity can be used to treat or prevent hyperproliferative
CC or benign dysproliferative disorders e.g. psoriasis and tissue
CC hypertrophy. Ribozymes or antisense Nogo nucleic acids can be used to
CC inhibit production of Nogo protein to induce regeneration of neurons or
CC to promote structural plasticity of the CNS in disorders where neurite
CC growth, regeneration or maintenance are deficient or desired.
CC The animal models can be used in diagnostic and screening methods for

Db	1555	GACAGCTCCAGAGCATATATTACCTGTGCTTCCTTTACCTCAGCAACCGAAAGCACCACA	1614
Qy	721	ACAAACATTTTTCCCTTGTGGAAGATCATACTTCGGAAAAATAAGACAGATGAAAAAAG	780
Db	1615	GCAAACACTTTCCCTTTGTTAGAAGATCATACTTCAGAAAAATAAAACAGATGAAAAAAA	1674
Qy	781	ATAGAA-AAAAAAGGCCACAAATTGTAACAGAGAAGAATGCAAGTGTCAAGACATCAAAC	839
Db	1675	ATAGAAGAAAGGAAGGCCCAAATTATAACAGAGAAGA---CTAGCCCCAAAACGTCAAAT	1731
Qy	840	CCTTTCCTTATGGCAGCACAGGAGTCTAAGACAGATTACGTTACAACAGATCATGTGTCA	899
Db	1732	CCTTTCCTTGTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCA	1791
Qy	900	AAGGTGACCGAGGAAGTAGTGGCAAACATGCCTGAAGGTCTAACCCCAGATTTGGTTTCAG	959
Db	1792	AAGGTGACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTTCAG	1851
Qy	960	GAAGCATGTGAAAGTGAATTGAATGAAGCTACTGGTACAAAAATTGCCTTTGAAACAAAA	1019
Db	1852	GAAGCATGTGAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAA	1911
Qy	1020	ATGGACCTGGTTCAAACCTTCAGAAGCTGTGCAGGAGTCACTTTACCCCTGTAACACAGCTT	1079
Db	1912	GTGGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAGCTT	1971
Qy	1080	TGCCCATCTTTTGAAGAATCTGAAGCTACTCCGTCACCGGTTTTGCCTGACATTGTCATG	1139
Db	1972	TGCCCATCATTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGCCTGATATTGTTATG	2031
Qy	1140	GAAGCACCATTAAATTCTGTAGTTCCTAGTGCTGGTGTCTTCTGCAGTGCAGCTCAGTTCA	1199
Db	2032	GAAGCACCATTAAATTCTCTCCTTCCAAGCGCTGGTGTCTTCTGTAGTGCAGCCAGTGTA	2091
Qy	1200	TCACCATTAGAACTCTTCCTTCAGTTAATTATGAAAGCATAAAGTTTGAGCCTGAAAAAT	1259
Db	2092	TCCCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAAC	2151
Qy	1260	CCCCACCATATGAGGAGGCCATGAATGTATCACTAAAAAAGAATCAGGAATGAATGAA	1319
Db	2152	CCCCACCATATGAAGAAGCCATGAATGTAGCACT---AAAAGCTTTGGGAACAAAGGAA	2208
Qy	1320	GAAATCACAGAGCCTGAAGGTATTAGTGTAGCTGTTTCAGGAAACAGAAGCTCCTTATATA	1379
Db	2209	GGAATAAAAGAGCCTGAAAGTTTTAATGCAGCTGTTTCAGGAAACAGAAGCTCCTTATATA	2268
Qy	1380	TCTATTGCATGTGATTTAATTAAAGAAACAAAGATCTCTACTGAACCGACTCCAGATTTTC	1439
Db	2269	TCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTTC	2328
Qy	1440	TCTAGTTATTTCAGAAATAGCAGAAGTTGCACAGCCAGTGCCCGAGCATTTCTGAGCTAGTT	1499
Db	2329	TCTAATTATTTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTG	2388
Qy	1500	GAAGATTCCTCCCCGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCCGAA	1559

Db 2389 GAGGATTCCCTCACCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTCGATTCCCTGAA 2448
 Qy 1560 GTTCCACAAAAACAAGATGAAGCTGTAATACTTGTGAAAGAAAACCTCACTGAAATTTCA 1619
 || ||||| ||||| || ||||| || || ||||| || || ||||| || ||
 Db 2449 GTCCACAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGAAGTGTC- 2507
 Qy 1620 TCTGAGTCAATGACAGGACATGACAATAAGGGAAAACCTCAGTGCTTCACCATCACCTGAG 1679
 | || || || |||| |||| || || |||| |||| || || ||||
 Db 2508 -----TGAGACAGTAGCCCAGCACAAAGAGGAGAGACTTAGTGCCCTCAC---CTCAGGAG 2559
 Qy 1680 GGAGGAAAACCGTATTTGGAGTCTTTTCAGCCCAGTTTAGGCATCACAAAAGATACCTTA 1739
 ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 2560 CTAGGAAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAAAAGATGC---T 2616
 Qy 1740 GCACCTGATGAAGTTTCAGCATTGACCCAAAAGGAGAAAATCCCTTTGCAGATGGAGGAG 1799
 ||| || |||| || || ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 2617 GCATCTAATGACATTCCAACATTGACCAAAAAGGAGAAAATTTCTTTGCAAATGGAAGAG 2676
 Qy 1800 CTCAATACTGCAGTTTATTCAAGTGATGGCTTATTCAATTGCTCAGGAAGCAAACCTAAGA 1859
 | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 2677 TTTAATACTGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGACAAAATAAAA 2736
 Qy 1860 GAAAGTGAAACATTTTCAGATTCACTCTCCGATTGAGATTATAGATGAGTTCCCGACCTTT 1919
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 2737 GAAAGTGAAACATTTTCAGATTCACTCTCCGATTGAGATAATAGATGAATTTCCACGTTT 2796
 Qy 1920 GTCAGTTCTAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACACTGACCTAGAAGTA 1979
 ||||| |||| | |||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 2797 GTCAGTGCTAA---AGATGATTCTCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTA 2853
 Qy 1980 GCCCACAAAAGTGAAATTGCTGACATCCAGGATG
 || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 2854 TCCGACAAAAGTGAAATTGCTAATATCCAAAGCGGGGCAGATTCAATTGCCTTGCTTAGAA 2913
 Qy 2040 TTGCCCCATGACCTTTCTTTCAAGAGTATACAACCTAAAGAGGAAGTTCATGTCCCAGAT 2099
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 2914 TTGCCCTGTGACCTTTCTTTCAAGAATATATATCCTAAAGATGAAGTACATGTTTCAGAT 2973
 Qy 2100 GAGTTCTCCAAAGATAGGGGTGATGTTTCAAAGGTGCCCCGTACTGCCTCCAGATGTTTCT 2159
 || ||||| || ||||| || ||||| || ||||| || ||||| || ||||| || |||||
 Db 2974 GAATTCTCCGAAAATAGGTCCAGTGATCTAAGGCATCCATATCGCCTTCAAATGTCTCT 3033
 Qy 2160 GCTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAAACCCAAAGTTCTTGTGAAAGAA 2219
 ||||| |||| |||| || ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 3034 GCTTTGGAACCTCAGACAGAAATGGGCAGCATAGTTAAATCCAAATCACTTACGAAAGAA 3093
 Qy 2220 GCCGAGAGAAAACCTTCCTTCTGATACAGAAAAAGAGCGAAGATCTCCATCTGCTATATTT 2279
 || |||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 3094 GCAGAGAAAAAATTCCTTCTGACACAGAGAAAGAGGACAGATCCCTGTGAGCTGTATTG 3153
 Qy 2280 TCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAG 2339
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 5Db 8863154 ~~GGAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAG~~ 2039
 Qy 2340 ACTGGAGTGGTGTGTTGGTGCCAGCTTGTTCTGCTGCTCTCGCTGACAGTATTCAGCATT 2399
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 3214 ACTGGAGTGGTGTGTTGGTGCCAGCTTATTCCTGCTGCTGTCTCTGACAGTGTTTCAGCATT 3273

Qy 2400 GTGAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATA 2459
 || |||||
 Db 3274 GTCAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATA 3333

Qy 2460 TATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATT CAGGGCATAT 2519
 |||||
 Db 3334 TATAAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCCACCCATT CAGGGCATAT 3393

Qy 2520 TTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTT CAGAAGTACAGCAATTCTGCTCTT 2579
 || |||||
 Db 3394 TTAGAATCTGAAGTTGCTATATCAGAGGAATTGGTT CAGAAATACAGTAATTCTGCTCTT 3453

Qy 2580 GGT CATGT TAACTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGTTGATGATTTAGTT 2639
 |||||
 Db 3454 GGT CATGTGAACAGCACAATAAAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTTAGTT 3513

Qy 2640 GATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTCAAT 2699
 |||||
 Db 3514 GATTCCCTGAAGTTTGCAGTGTTGATGTGGGTGTTTACTTATGTTGGTGCCTTGTTCAAT 3573

Qy 2700 GGTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCCTGTTATTTATGAA 2759
 |||||
 Db 3574 GGTCTGACACTACTGATTTTAGCTCTGATCTCACTCTTCAGTATTCTGTTATTTATGAA 3633

Qy 2760 CGGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTTAAAGATGCT 2819
 |||||
 Db 3634 CGGCATCAGGTGCAGATAGATCATTATCTAGGACTTGCAAACAAGAGTGTTAAGGATGCC 3693

Qy 2820 ATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGAGAAAGCCTG 2879
 ||||| a |||ps 14;
 Db 3694 ATGGCCAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCAGATTGAAAAAGCCCC 3753

Qy 2880 AAAGAGTTAACAATAGAGGAGTTTATCTTTAAAGGGGATATTCATTGATTCCATTGGGG 2939
 ||
 Db 3754 AA-----ACAGAAGTTCATCTTTAAAGGGGACACTCACTTGATTAC---GGG 3797

Qy 2940 AGGGTCAGGGAAGAACAAGCCTTGACATTGCAGTGCAGTTTCACAGATCTTTATTTT 2999
 || |||||
 Db 3798 GGTGGGAGGGTCAGGGGTGAGCCCTTGGTGGCCGTGCGGTTT--CAGCTCTTTATTTT 3855

Qy 3000 GCAACGCAGTGTCTGAGGAAAAATGACCTGTCTTGACTGCCCTGTGTTTCATCATCTTAAG 3059
 ||| ||| |||||
 Db 3856 GCAGTGCAGTGTCTGAGGAAAAATTACCTGTCTTGACTT-CCTGTGTTTATCATCTTAAG 3914

Qy 3060 TATTGTAAGCTGCTATGTATGGATTTAAATCGTAATCATATTTGTTTTCTGTATGAGG 3119
 |||||
 Db 3915 TATTGTAAGCTGCTGTGTATGGATCT-CATTGTAGTCACACTTGTCTTCCCCAATGAGGC 3973

Qy 3120 CACTGGTGAATAAAACAAAGATCTGAGAAAGCTGTATATTACACTTTGTGCGAGGTAGTCT 3179
 |||||
 Db 3974 GCCTGGTGAATAAAAGGA--CTCGGGGAAAGCTGTGCATTGTATCTGCTGCAGGGTAGTCT 4031

Qy 3180 TGCTGTATTTGGGGAATTGCAAAGAAAGTGGAGCT--GACAGAAATAACCTTTT CACA 3236
 |||||
 Db 4032 AGCTGTATGCAGAGAGTTGTAAAGAAGGCAAATCTGGGGGCAGGGAAAACCTTTT CACA 4091

KW vulnerary; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant;
 KW nootropic; antiparkinsonian; ophthalmological; analgesic; hepatotropic;
 KW osteopathic; vasotropic; nephrotropic; cytostatic; antigen; gene therapy;
 KW neurotransmitter receptor; rat; gene; ds.
 XX
 OS Rattus norvegicus.
 XX
 FH Key Location/Qualifiers
 FT CDS 253..3744
 FT /*tag= a
 FT /product= "Nogo-A"
 XX
 PN US2002072493-A1.
 XX
 PD 13-JUN-2002.
 XX
 PF 28-JUN-2001; 2001US-0893348.
 XX
 PR 19-MAY-1998; 98IL-0124500.
 PR 21-JUL-1998; 98WO-US14715.
 PR 22-DEC-1998; 98US-0218277.
 PR 19-MAY-1999; 99US-0314161.
 XX
 PA (YEDA) YEDA RES & DEV CO LTD.
 XX
 PI Eisenbach-Schwartz M, Hauben E, Cohen IR, Beserman P, Mosonego A;
 PI Moalem G;
 XX
 DR WPI; 2002-607255/65.
 DR P-PSDB; ABB81074, ABB81076, ABB81077.
 XX
 PT Promoting nerve regeneration and preventing neuronal degeneration in
 PT the central/peripheral nervous system from injury/disease, comprises
 PT administering nervous system-specific activated T cells/antigen, or
 PT analogs/peptides -
 XX
 PS Disclosure; Page 40-44; 93pp; English.
 XX
 CC The invention relates to promoting nerve regeneration or conferring
 CC neuroprotection and preventing or inhibiting neuronal degeneration in the
 CC central/peripheral nervous system (NS). The method involves administering
 CC NS-specific activated T cells, NS-specific antigen, its analogue or its
 CC peptide, a nucleotide sequence the NS-specific antigen or its analogue or
 CC combinations. The method is useful for promoting nerve regeneration and
 CC preventing neuronal degeneration in central/peripheral nervous system
 CC from injury/disease, where the injury is spinal cord injury, blunt
 CC trauma, penetrating trauma, hemorrhagic stroke, ischaemic stroke or
 CC damages caused by surgery such as tumour excision. The disease is not an
 CC autoimmune disease or neoplasm. The disease results in a degenerative
 CC process occurring in either gray or white matter or both. The disease
 CC is diabetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's
 CC disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea,
 CC amyotrophic lateral sclerosis, non-arteritic optic neuropathy, and
 CC vitamin deficiency, intervertebral disc herniation, prion diseases such
 CC as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral
 CC neuropathies associated with various diseases, including but not limited
 CC to uremia, porphyria, hypoglycemia, Sjorgren Larsson syndrome, acute

CC sensory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary
 CC amyloidosis, obstructive lung diseases, acromegaly, malabsorption
 CC syndromes, polycythemia vera, immunoglobulin (Ig)A- and IgG gamma-
 CC pathies, complications of various drugs (e.g., metronidazole) and toxins
 CC (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia
 CC telangectasia, Friedreich's ataxia, amyloid polyneuropathies,
 CC adrenomyeloneuropathy, Giant axonal neuropathy, Refsum's disease, Fabry's
 CC disease, or lipoproteinemia. The present sequence represents a DNA
 CC encoding the rat neurotransmitter receptor protein Nogo (Nogo-A, Nogo-B
 CC and Nogo-C), an example of NS-specific antigen.

XX

SQ Sequence 4684 BP; 1358 A; 1047 C; 1112 G; 1167 T; 0 other;

Query Match 56.9%; Score 2179.4; DB 24; Length 4684;
 Best Local Similarity 78.2%; Pred. No. 0;
 Matches 3008; Conservative 0; Mismatches 731; Indels 110; Gaps 28;

Qy	1	CTATCTCTCTCTCAGCCGCTGCTTTTAAAGAACGTGAATACCTTGGTGATTTACCAGCA	60
Db	928	CTATCTCTCTCTCAACTGTTTCTTTTAAAGAACATGGATACCTTGGTAACTTATCAGCA	987
Qy	61	GTACTGCCCCACTGAAGGAACACTTCCAGCAACTTCAAATGAAGCTTCTAAAGCATTCTCA	120
Db	988	GTGTCATCCTCAGAAGGAACAATTGAAGAACTTTAAATGAAGCTTCTAAAGAGTTGCCA	1047
Qy	121	GAGAAGGCCAAAAATCCATTTGTAGAGAGAAATTTAACAGAATTTTCAGAATTGGAATAT	180
Db	1048	GAGAGGGCAACAAATCCATTTGTAAATAGAGATTTAGCAGAATTTTCAGAATTAGAATAT	1107
Qy	181	TCAGAAATGGAATCATCATTCAGTGGCTCTCAAAGGCAGAACCTGCCGTAACAGTAGCG	240
Db	1108	TCAGAAATGGGATCATCTTTTAAAGGCTCCCCAAAAGGAGAGTCAGCCATATTAGTAGAA	1167
Qy	241	AATCCTAGGGACGAAATAGTTGTGAGGAGTAGAGATAAAGAAGAGGACTTAGTTAGTCTT	300
Db	1168	AACACTAAGGAAGAAGTAATTGTGAGGAGTAAAGACA---AAGAGGATTTAGTTTGTAGT	1224
Qy	301	AACATCCTTCATACTCAGCAGGAGTTATCTACAGTCCTTACGAAATCAGTTGAAGAAGAA	360
Db	1225	GCAGCCCTTCACAGTCCACAAGAATCACCT-----GTGGGTAAAGAA	1266
Qy	361	GATAGAGTTTCTGTCTCCAGAAAAAACAAGGACAGTTTTTAAGGAAAAGGGAGTTGCAGCA	420
Db	1267	GACAGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTAAATGAAATGCAGATGTCAGTA	1326
Qy	421	GAAGCTTCTATGGGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG	480
Db	1327	GTAGCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGGGAAGTG	1386
Qy	481	AAAGATACTTACAAGCAAGATAGTGATGTTTTGATTGCTGGAGGTAATATAGAGAGCAAA	540
Db	1387	AAAGATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCTAAT-----	1434
Qy	541	TTGGAAGGTAAAGTGGATAAGAAACACTTTTCAGATAGCCTTGAACAAACAAATCGTGAA	600
Db	1435	GTGGAAGTAAAGTGGACAGAAAATGCTTGAAGATAGCCTGGAGCAAAAAGTCTTGGG	1494

Qy125X	601	AAAGATAGTGAAAGCAGTAATGATGACACTTCAATTTCCCACTACACCGAAAGCTGTAAAG	660
Db	1495	AAGGATAGTGAAAGGCAGAAATGAGGATGCTTCTTTCCCCAGTACCCAGAACCTGTGAAG	1554
Qy	661	GGTGGTTCCGGAGCGTACATCACGTGTGCTCCCTTTAACCCAAACAACCTGAGAATGTTTCA	720
Db	1555	GACAGCTCCAGAGCATATATTACCTGTGCTTCCTTTACCTCAGCAACCGAAAGCACCACA	1614
Qy	721	ACAAACATTTTTCCCTTGTTGGAAGATCATACTTCGGAAAATAAGACAGATGAAAAAAG	780
Db	1615	GCAAACACTTTCCCTTGTTAGAAAGATCATACTTCAGAAAATAAAACAGATGAAAAAAG	1674
Qy	781	ATAGAA -AAAAAAGGCACAAATTGTAACAGAGAAGAATGCAAGTGTCAAGACATCAAAC	839
Db	1675	ATAGAAGAAAGGAAGGCCAAATTATAACAGAGAAGA ---CTAGCCCCAAACCGTCAAAT	1731
Qy	840	CCTTTCCTTATGGCAGCACAGGAGTCTAAGACAGATTACGTTACAACAGATCATGTGTCA	899
Db	1732	CCTTTCCTTGTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCA	1791
Qy	900	AAGGTGACCGAGGAAGTAGTGGCAAACATGCCTGAAGGTCTAACCCAGATTTGGTTCAG	959
Db	1792	AAGGTGACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTCAG	1851
Qy	960	GAAGCATGTGAAAGTGAATTGAATGAAGCTACTGGTACAAAAATTGCCTTTGAAACAAAA	1019
Db	1852	GAAGCATGTGAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAA	1911
Qy	1020	ATGGACCTGGTTCAAACCTTCAGAAGCTGTGCAGGAGTCACTTTACCCTGTAACACAGCTT	1079
Db	1912	GTGGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAGCTT	1971
Qy	1080	TGCCCATCTTTTGAAGAATCTGAAGCTACTCCGTACCCGTTTTGCCTGACATTGTCATG	1139
Db	1972	TGCCCATCATTTGAGGAAGCTGAAGCAACTCCGTACCCAGTTTTGCCTGATATTGTTATG	2031
Qy	1140	GAAGCACCATTAAATTCTGTAGTTCCTAGTGCTGGTGCTTCTGCAGTGCAGCTCAGTTCA	1199
Db	2032	GAAGCACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCAGTGTA	2091
Qy	1200	TCACCATTAGAACTCTTCCTTCAGTTAATTATGAAAGCATAAAGTTTGAGCCTGAAAAAT	1259
Db	2092	TCCCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAAAC	2151
Qy	1260	CCCCCACCATATGAGGAGGCCATGAATGTATCACTAAAAAAGAATCAGGAATGAATGAA	1319
Db	2152	CCCCCACCATATGAAGAAGCCATGAATGTAGCACT ---AAAAGCTTTGGGAACAAAGGAA	2208
Qy	1320	GAAATCACAGAGCCTGAAGGTATTAGTGTAGCTGTTCAGGAAACAGAAGCTCCTTATATA	1379
Db	2209	GGAATAAAAGAGCCTGAAAGTTTTAATGCAGCTGTTCAGGAAACAGAAGCTCCTTATATA	2268
Qy	1380	TCTATTGCATGTGATTTAATTAAAGAAACAAAGATCTCTACTGAACCGACTCCAGATTTT	1439
Db	2269	TCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTT	2328
Qy	1440	TCTAGTTATTTCAGAAATAGCAGAAGTTGCACAGCCAGTGCCCCGAGCATTCTGAGCTAGTT	1499

[illegible]

Db 3154 TCAGCAGAGCTGAGTAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAG 3213
 Qy 2340 ACTGGAGTGGTGTGTTGGTGCCAGCTTGTTCCTGCTGCTCTCGCTGACAGTATTCAGCATT 2399
 |||||
 Db 3214 ACTGGAGTGGTGTGTTGGTGCCAGCTTATTCCTGCTGCTGTCTCTGACAGTGTTCAGCATT 3273
 Qy 2400 GTGAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATA 2459
 ||
 Db 3274 GTCAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATA 3333
 Qy 2460 TATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATTTCAGGGCATAT 2519
 |||||
 Db 3334 TATAAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCCACCCATTTCAGGGCATAT 3393
 Qy 2520 TTGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGCAATTCTGCTCTT 2579
 ||
 Db 3394 TTAGAATCTGAAGTTGCTATATCAGAGGAATTGGTTCAGAAATACAGTAATTCTGCTCTT 3453
 Qy 2580 GGTCAATGTTAACTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGTTGATGATTTAGTT 2639
 |||||
 Db 3454 GGTCAATGTGAACAGCACAATAAAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTTAGTT 3513
 Qy 2640 GATTCTCTGAAGTTTGCAGTGTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTCAAT 2699
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 Db 3514 GATTCCCTGAAGTTTGCAGTGTGATGTGGGTGTTTACTTATGTTGGTGCCTTGTTCAAT 3573
 Qy 2700 GGTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCTGTATTATTTATGAA 2759
 |||||
 Db 3574 GGTCTGACACTACTGATTTTAGCTCTGATCTCACTCTTCAGTATTCCTGTATTATTTATGAA 3633
 Qy 2760 CGGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGT GATGCT 2819
 |||||
 Db 3634 CGGCATCAGGTGCAGATAGATCATTATCTAGGACTTGCAAACAAGAGTGTTAAGGATGCC 3693
 Qy 2820 ATGGCTAAAATCCAAGCAAAATCCCTGGATTGAAGCGTAAAGCTGAATGAGAAAGCCTG 2879
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 Db 3694 ATGGCCAAAATCCAAGCAAAATCCCTGGATTGAAGCGCAAAGCAGATTGAAAAGCCCC 3753
 Qy 2880 AAAGAGTTAACAATAGAGGAGTTTATCTTTAAAGGGGATATTCATTTGATTCCATTGGGG 2939
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 Db 3754 AA-----ACAGAAGTTCATCTTTAAAGGGGACACTCACTTGATTAC---GGG 3797
 Qy 2940 AGGGTCAGGGAAGAACAAGCCTTGACATTGCAGTGCAGTTTCACAGATCTTTATTTTAA 2999
 ||
 Db 3798 GGTGGGAGGGTCAGGGGTGAGCCCTTGGTGGCCGTGCGGTTT--CAGCTCTTTATTTTAA 3855
 Qy 3000 GCAACGCA0X| GAGGAAAAATGACCTGTCTTGACTGCCCTGTGTTTCATCTTTAAG 3059
 |||||
 Db 3856 GCAGTGCAGTGTGTTGAGGAAAAATTACCTGTCTTGACTT-CCTGTGTTTATCATCTTAAG 3914
 Qy 3060 TATTGTAAGCTGCTATGTATGGATTTAAATCGTAATCATATTTGTTTTCTGTATGAGG 3119
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 Db 3915 TATTGTAAGCTGCTGTGTATGGATCT-CATTGTAGTCACACTTGTCTTCCCAATGAGGC 3973
 Qy 3120 CACTGGTGAATAAAACAAGATCTGAGAAAGCTGTATATTACACTTTGTGCGAGGTAGTCT 3179
 |||||
 Db 3974 GCCTGGTGAATAAAGGA--CTCGGGGAAAGCTGTGCATTGTATCTGCTGCAGGGTAGTCT 4031

XX
 DE Human secreted protein BG160_1 cDNA.
 XX
 KW BG160_1; secreted protein; protein factor; human; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 102..2030
 FT /*tag= a
 FT sig_peptide 1863..1899
 FT /*tag= b
 FT /note= "putative leader/signal peptide"
 FT mat_peptide 1900..2027
 FT /*tag= c
 XX
 PN WO9817687-A2.
 XX
 PD 30-APR-1998.
 XX
 PF 24-OCT-1997; 97WO-US19590.
 XX
 PR 24-OCT-1997; 97US-0740274.
 PR 25-OCT-1996; 96US-0740274.
 XX
 PA (GEMY) GENETICS INST INC.
 XX
 PI Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Merberg D;
 PI Racie LA, Spaulding V, Treacy M;
 XX
 DR WPI; 1998-261426/23.
 DR P-PSDB; AAW58383.
 XX
 PT Nucleic acid encoding secreted protein from human cells - useful,
 PT e.g. as immunomodulator, antitumour agent, promoters of tissue
 PT growth, haemostatic and thrombolytic agents etc.
 XX
 PS Claim 20; Page 74-75; 114pp; English.
 XX
 CC This cDNA clone, designated BG160_1, codes for a novel human
 CC secreted protein (see AAW58383). It was isolated from a human adult
 CC brain cDNA library using methods selective for cDNAs that encode
 CC secreted proteins. The clone is deposited in composite clone
 CC ATCC 98232; an oligonucleotide (see AAT99725) is designed to isolate
 CC the clone from the composite. The predicted AT415_4 amino acid
 CC sequence shows homology to neuroendocrine-specific proteins. Novel
 CC cDNA clones (see AAV30916-32) coding for human secreted proteins (see
 CC AAW58580-90) are claimed. These can be used for recombinant
 CC production of the secreted proteins for analysis, characterisation,
 CC diagnostic or therapeutic use. They can also be used as tissue or
 CC mol.wt. markers, for chromosome identification, to identify genetic
 CC disorders, to isolate new related DNA, as sources of primers for
 CC PCR, to generate antibodies, and in interaction trap assays. The
 CC secreted proteins may also have many biological activities, e.g.
 CC cytokine, immunomodulator, haematopoiesis regulating activity,
 CC tissue growth activity, activin or inhibin activity, chemotactic or
 CC chemokinetic activity, haemostatic and thrombolytic activity,

CC receptor/ligand activity, antiinflammatory, cadherin and tumour
CC invasion suppressor activity, and tumour inhibition activity. The
CC proteins can be expressed in vivo from DNA, introduced in gene
CC therapy vectors.

XX

SQ Sequence 2386 BP; 756 A; 450 C; 494 G; 686 T; 0 other;

Query Match 46.4%; Score 1777.2; DB 19; Length 2386;
Best Local Similarity 86.9%; Pred. No. 0;
Matches 2101; Conservative 0; Mismatches 258; Indels 59; Gaps 11;

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Qy      827 CAAGACATCAAACCCCTTTCCTTATGGCAGCACAGGAGTCTAAGACAGATTACGTTACAAC 886
      ||| ||||| ||||| ||| | ||||| ||||| ||| ||||| ||| |||||
Db      2   CAAAACATCAAACCCCTTTCCTGTAGCAGCACAGGATTCTGAGACAGATTATGTCAAC 61

Qy      887 AGATCATGTGTCAAAGGTGACCGAGGAAGTAGTGGCAAACATGCCTGAAGGTCTAACCCC 946
      |||| | | | ||||| ||||| ||||| ||||| ||||| ||| | | |
Db      62  AGATAATTTAACAAAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCC 121

Qy      947 AGATTTGGTTCAGGAAGCATGTGAAAGTGAATTGAATGAAGCTACTGGTACAAAAATTGC 1006
      ||||| | | ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      122 AGATTTAGTACAGGAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGC 181

Qy     1007 CTTTGAAACAAAAATGGACCTGGTTCAAACCTTCAGAAGCTGTGCAGGAGTCACTTTACCC 1066
      | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      182 TTATGAAACAAAAATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCC 241

Qy     1067 TGTAACACAGCTTTGCCCATCTTTTGAAGAATCTGAAGCTACTCCGTCACCGGTTTTGCC 1126
      || | ||||| ||||| ||||| ||| ||||| ||||| ||||| ||||| |||||
Db      242 TGCAGCACAGCTTTGCCCATCATTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGCC 301

Qy     1127 TGACATTGTCATGGAAGCACCATTAAATTCGTAGTTCTTAGTGCTGGTGCTTCTGCAGT 1186
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |
Db      302 TGACATTGTTATGGAAGCACCATTGAATTCGCAGTTCTTAGTGCTGGTGCTTCCGTGAT 361

Qy     1187 GCAGCTCAGTTCATCACCATTAGAACTCTTCCTTCAGTTAATTATGAAAGCATAAAGTT 1246
      |||| | | ||||| ||||| ||| | ||||| ||||| ||||| ||||| |||||
Db      362 ACAGCCCAGCTCATCACCATTAGAAGC---TTCTTCAGTTAATTATGAAAGCATAAAACA 418

Qy     1247 TGAGCCTGAAAATCCCCCACCATATGAGGAGGCCATGAATGTATCACTAAAAAAGAATC 1306
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      419 TGAGCCTGAAAACCCCCCACCATATGAAGAGGCCATGAGTGATCACTAAAAAAGTATC 478

Qy     1307 AGGAATGAATGAAGAAATCACAGAGCCTGAAGGTATTAGTGTAGCTGTTCAGGAAACAGA 1366
      ||||| | | ||||| | ||||| ||||| ||||| ||| ||||| ||||| |||||
Db      479 AGGAATAAAGGAAGAAATTAAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGA 538

Qy     1367 AGCTCCTTATATATCTATTGCATGTGATTTAATTAAAGAAACAAAGATCTCTACTGAACC 1426
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      539 AGCTCCTTATATATCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACC 598

Qy     1427 GACTCCAGATTTCTCTAGTTATTTCAGAAATAGCAGAAGTTGCACAGCCAGTGCCCGAGCA 1486
      |||| | ||||| ||||| ||||| ||| ||||| ||||| ||||| ||||| |||||
Db      599 AGCTCCGATTTCTCTGATTATTTCAGAAATGGCAAAGTTGAACAGCCAGTGCCCTGATCA 658

Qy     1487 TTCTGAGCTAGTTGAAGATTCCTCCCCCGATTCTGAACCAGTTGACTTATTTAGTGATGA 1546
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Accession	Gene	Strain	Position	Sequence	Length
Db	659	TTCTGAGCTAGTTGAAGATTCCCTCACCTGATTCTGAACCAAGTTGACTTATTTAGTGATGA	718		
Qy	1547	TTCAATACCCGAAGTTCCACAAAAACAAGATGAAGCTGTAATACTTGTGAAAGAAAACCT	1606		
Db	719	TTCAATACCTGACGTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCT	778		
Qy	1607	CAC TGAAATTT CATCTGAGTCAATGACAGGACATGACAATAAGGGAAAAC TCAGTGCTTC	1666		
Db	779	CAC TGAGACTT CATTTGAGTCAATGATAGAATATGAAAATAAGGAAAAAC TCAGTGCTTT	838		
Qy	1667	ACCATCACCTGAGGGAGGAAAAACCGTATTTGGAGTCTTTTCAGCCCAGTTTAGGCATCAC	1726		
Db	839	GC---CACCTGAGGGAGGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACAC	895		
Qy	1727	AAAAGATACCTTAGCACCTGATGAAGTTTCAGCATTGACCCAAAAGGAGAAAAATCCCTTT	1786		
Db	896	AAAAGATACCTGTACCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAAATTCCTTT	955		
Qy	1787	GCAGATGGAGGAGCTCAATACTGCAGTTTATTCAAGTGATGGCTTATTCATTGCTCAGGA	1846		
Db	956	GCAGATGGAGGAGCTCAGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGA	1015		
Qy	1847	AGCAAACCTAAGAGAAAGTGAAACATTTTCAGATT CATCTCCGATTGAGATTATAGATGA	1906		
Db	1016	AGCACAGATAAGAGAAACTGAAACGTTTTCAGATT CATCTCCAATTGAAATATATAGATGA	1075		
Qy	1907	GTTCCCGACCTTTGTGTCAGTTCTAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACAC	1966		
Db	1076	GTTCCCTACATTGATCAGTTCTAAAAGTGAATTCATTTTCTAAATTAGCCAGGGAATATAC	1135		
Qy	1967	TGACCTAGAAGTAGCCCAAAAAGTGAAATTGCTGACATCCAGGATGGT GTCATT	2026		
Db	1136	TGACCTAGAAGTATCCCAAAAAGTGAAATTGCTAATGCCCGGATGGAGCTGGGTCATT	1195		
Qy	2027	GGCTTGTGCAGGATTGCCCCATGACCTTTCTTTCAAGAGTATACAACCTAAAGAGGAAGT	2086		
Db	1196	GCCTTGACAGAATTGCCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGA	1255		
Qy	2087	TCA-----TGTC CAGATGAGTTCTCCAAAGATAGGGGTGATGTTTCAAAGGTGCCCGT	2140		
Db	1256	GAAAATCAGTTTCTCAGATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTT	1315		
Qy	2141	ACTGCCTCCAGATGTTTCTGCTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAAACC	2200		
Db	1316	ATTGCCTCCAGATGTTTCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACC	1375		
Qy	2201	CAAAGTTCTTGTGAAAGAAGCCGAGAGAAAAC TCCTTCTGATACAGAAAAAGAGCGAAG	2260		
Db	1376	CAAAGTTCTTGTGAAAGAAGCTGAGAAAAAAC TCCTTCCGATACAGAAAAAGAGGACAG	1435		
Qy	2261	ATCTCCATCTGCTATATTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTA	2320		
Db	1436	ATCACCATCTGCTATATTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTGTA	1495		
Qy	2321	CTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTGTTCCCTGCTGCTCTC	2380		
Db	1496	CTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTCCTGCTGCTTTC	1555		

Qy	2381	GCTGACAGTATTTCAGCATTGTGAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCTGT	2440
Db	1556	ATTGACAGTATTTCAGCATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGT	1615
Qy	2441	GACTATCAGCTTTAGGATATATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGG	2500
Db	1616	GACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGG	1675
Qy	2501	CCACCCATTTCAGGGCATATTTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTTCAGAA	2560
Db	1676	CCACCCATTTCAGG-----GAAGTTGCTATATCTGAGGAGTTGGTTTCAGAA	1720
Qy	2561	GTACAGCAATTCTGCTCTTGGTCATGTTAACTGCACAATAAAAGAACTCAGACGCCTCTT	2620
Db	1721	GTACAGTAAATCTGCTCTTGGTCATGTGAAGTGCACGATAAAGGAACTCAGGCGCCTCTT	1780
Qy	2621	CTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGAGTGTGGGTATTTACCTA	2680
Db	1781	CTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGAGTGTGGGTATTTACCTA	1840
Qy	2681	TGTTGGTGCCTTGTTCAATGGTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAG	2740
Db	1841	TGTTGGTGCCTTGTTAATGGTCTGACACTACTGATTTTGGCTCTCATTTCCTCTTCAG	1900
Qy	2741	TGTTCCCTGTTATTTATGAACGGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAA	2800
Db	1901	TGTTCCCTGTTATTTATGAACGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAA	1960
Qy	2801	TAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAA	2860
Db	1961	TAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAA	2020
Qy	2861	AGCTGAATGAGAAAGCCTGAAAGAGTTAACAATAGAGGAGTTTATCTTTAAAGGGGATAT	2920
Db	2021	AGCTGAATGAAAACGCCCAAAATAATTA-----GTAGGAGTTCATCTTTAAAGGGGATAT	2075
Qy	2921	TCATTTGATTCCATTGGGGAGGGTCAGGGAAGAACAAAGCCTTGACATTGCAGTGCAGTT	2980
Db	2076	TCATTTGATTATACGGGGAGGGTCAGGGAAGAACGAA-CCTTGACGTTGCAGTGCAGTT	2134
Qy	2981	TCAC-----AGATCTTTATTTTTAGCAACGCAGTG-TCTGAGGAAAAATGACCT	3028
Db	2135	TCACAGATCGTTGTTAGATCTTTATTTTTAGCCATGCACTGTTGTGAGGAAAAATTACCT	2194
Qy	3029	GTCTTGACTGCCCTGTGTTTCATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTAAAA	3088
Db	2195	GTCTTGACTGCCATGTGTTTCATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTAAAA	2254
Qy	3089	TCGTAATCATATTTGTTTTCTGTATGAGGCACTGGTGAATAAACAAAGATCTGAGAAA	3148
Db	2255	CCGTAATCATA--TCTTTTCTATCTGAGGCACTGGTGA-----ATAAAAAA	2301
Qy	3149	GCTGTATATTACACTTTGTGCGAGGTAGTCTTGCTGTAT-TTGGGGAATTGCAAAGAAAG	3207
Db	2302	CCTGTATATTTTACTTTGTGTCAGATAGTCTTGCCGCATCTTGGCAAGTTGCAGAGATGG	2361

Qy 3208 TGGAGCTGACAGAAATAA 3225
 ||||| | |||
 Db 2362 TGGAGCTAGAAAAAAAAA 2379

RESULT 14

AAF98399

ID AAF98399 standard; cDNA; 2386 BP.

XX

AC AAF98399;

XX

DT 07-JUN-2001 (first entry)

XX

DE Human cDNA clone BG160_1 sequence SEQ ID 41.

XX

KW Human; secreted protein; nutrient; cytokine modulator; proliferation;
 KW differentiation; immune system modulator; tissue growth; chemotactic;
 KW haemostatic; thrombolytic; anti-inflammatory; tumour inhibition; ss;
 KW haematopoiesis.

XX

OS Homo sapiens.

XX

PN WO200119988-A1.

XX

PD 22-MAR-2001.

XX

PF 14-SEP-2000; 2000WO-US25135.

XX

PR 17-SEP-1999; 99US-0398829.

XX

PA (GEMY) GENETICS INST INC.

XX

PI Jacobs K, McCoy JM, LaVallie ER, Collins-Racie LA, Evans C;

PI Merberg D, Treacy M, Bowman MR, Spaulding V, tino M|||

XX

DR WPI; 2001-244801/25.

DR P-PSDB; AAB90682.

XX

PT Isolated nucleic acids encoding polypeptides, useful for modulating

PT e.g. cytokine and cell proliferation/differentiation activity, the

PT immune system and hematopoiesis regulating activity -

XX

PS Claim 1; Page 408-409; 557pp; English.

XX

CC Human cDNA clones represented in AAF98374 - AAF98489 encode secreted
 CC proteins AAB90667 - AAB90750. The cDNA clones are isolated from various
 CC tissue types, and may be used in the prevention, treatment and diagnosis
 CC of diseases associated with inappropriate protein expression. The
 CC polypeptides and nucleic acids may be used as nutrients or to modulate
 CC cytokine and cell proliferation/differentiation activity and may also be
 CC involved in modulation of the immune system. The cDNA sequences,
 CC proteins, their agonists and/or antagonists exhibit haematopoiesis
 CC regulating activity; tissue growth activity; activin/inhibin activity;
 CC chemotactic/chemokinetic activity; haemostatic and thrombolytic
 CC activity; receptor/ligand activity; anti-inflammatory activity;
 CC haematopoiesis activity; cadherin/tumour suppressor activity; and/or
 CC tumour inhibition activity. Included in the invention are probes

CC represented in AAF98490 - AAF98572 which are specific for the cDNA clones
CC encoding the secreted proteins.

XX

SQ Sequence 2386 BP; 756 A; 448 C; 496 G; 686 T; 0 other;

Query Match 46.3%; Score 1774; DB 22; Length 2386;
Best Local Similarity 86.8%; Pred. No. 0;
Matches 2099; Conservative 0; Mismatches 260; Indels 59; Gaps 11;

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Qy      827 CAAGACATCAAACCCCTTTCCTTATGGCAGCACAGGAGTCTAAGACAGATTACGTTACAAC 886
      ||| ||||||||||||||| ||| | ||||||||||| ||| ||||||||||| ||| |||||
Db       2 CAAAACATCAAACCCCTTTTCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAAC 61

Qy      887 AGATCATGTGTCAAAGGTGACCGAGGAAGTAGTGGCAAACATGCCTGAAGGTCTAACCCC 946
      |||| | | | ||||||||||| ||||||| ||||||||||||||||||| ||| |||
Db      62 AGATAATTTAACAAAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCC 121

Qy     947 AGATTTGGTTCAGGAAGCATGTGAAAGTGAATTGAATGAAGCTACTGGTACAAAAATTGC 1006
      ||||| || ||||||||||||||| ||||||| ||||||||||||||| |||||
Db     122 AGATTTAGTACAGGAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGC 181

Qy    1007 CTTTGAAACAAAAATGGACCTGGTTCAAACCTCAGAAGCTGTGCAGGAGTCACTTTACCC 1066
      | ||||||||||||||| ||||||| ||||||| | ||| |||||||
Db    182 TTATGAAACAAAAATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCC 241

Qy    1067 TGTAACACAGCTTTTGCCCATCTTTTGAAGAATCTGAAGCTACTCCGTCACCGGTTTTGCC 1126
      || | ||||||||||||||| ||||||| || ||||||||||| ||||| |||||||
Db    242 TGCAGCACAGCTTTTGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGCC 301

Qy    1127 TGACATTGTTCATGGAAGCACCATTAAATTCTGTAGTTCCTAGTGCTGGTGCTTCTGCAGT 1186
      ||||||| ||||||||||||||| ||||||| ||||||||||||||||||| |||
Db    302 TGACATTGTTATGGAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGAT 361

Qy    1187 GCAGCTCAGTTCATCACCATTAGAACTCTTCCTTCAGTTAATTATGAAAGCATAAAGTT 1246
      |||| | | ||||||||||||||| | |||||||||||||||||||
Db    362 ACAGCCCAGCTCATCACCATTAGAAGC---TTCTTCAGTTAATTATGAAAGCATAAAACA 418

Qy    1247 TGAGCCTGAAAATCCCCCACCATATGAGGAGGCCATGAATGTATCACTAAAAAAGAATC 1306
      ||||||| || ||||||||||| ||||||| ||||||| ||||| |||||
Db    419 TGAGCCTGAAAACCCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATC 478

Qy    1307 AGGAATGAATGAAGAAATCAGAGAGCCTGAAGGTATTAGTGTAGCTGTTTCAGGAAACAGA 1366
      ||||| || ||||||| | ||||||| ||||| || ||| ||||| |||||
Db    479 AGGAATAAAGGAAGAAATTAAAGAGCCTGAAAAATATTAATGCAGCTCTTCAAGAAACAGA 538

Qy    1367 AGCTCCTTATATATCTATTGCATGTGATTTAATTAAAGAAACAAAGATCTCTACTGAACC 1426
      ||||||| ||||||||||||||| ||||||| ||||||||||||||| ||| |||||
Db    539 AGCTCCTTATATATCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACC 598

Qy    1427 GACTCCAGATTTCTCTAGTTATTTCAGAAATAGCAGAAGTTGCACAGCCAGTGCCCCGAGCA 1486
      |||| ||||||| ||||||||||| || ||||||| ||||||||||| |||
Db    599 AGCTCCGATTTCTCTGATTATTTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCCTGATCA 658

Qy    1487 TTCTGAGCTAGTTGAAGATTCCTCCCCGATTCTGAACCAGTTGACTTATTTAGTGATGA 1546
      ||||||| ||||||||||| || ||||||| |||||||||||
Db    659 TTCTGAGCTAGTTGAAGATTCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGA 718
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Qy	1547	TTCAATATCCCGAAGTTCACACAAAAACAAGATGAAGCTGTAATACTTGTGAAAGAAAACCT	1606
Db	719	TTCAATACCTGACGTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCT	778
Qy	1607	CACTGAAATTTTCATCTGAGTCAATGACAGGACATGACAATAAGGGAAAACTCAGTGCTTC	1666
Db	779	CACTGAGACTTCATTTGAGTCAATGATAGAAATATGAAAAATAAGGAAAAACTCAGTGCTTT	838
Qy	1667	ACCATCACCTGAGGGAGGAAAACCGTATTTGGAGTCTTTTCAGCCCAGTTTAGGCATCAC	1726
Db	839	GC---CACCTGAGGGAGGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACAC	895
Qy	1727	AAAAGATACCTTAGCACCTGATGAAGTTTCAGCATTGACCCAAAAGGAGAAAATCCCTTT	1786
Db	896	A TACCCAGTTACCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAATTCCTTT	955
Qy	1787	GCAGATGGAGGAGCTCAATACTGCAGTTTATTCAAGTGATGGCTTATTTCATTGCTCAGGA	1846
Db	956	GCAGATGGAGGAGCTCAGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGA	1015
Qy	1847	AGCAAACCTAAGAGAAAGTGAAACATTTTCAGATTTCATCTCCGATTGAGATTATAGATGA	1906
Db	1016	AGCACAGATAAGAGAAACTGAAACGTTTTCAGATTTCATCTCCAATTGAAATTATAGATGA	1075
Qy	1907	GTTCCCGACCTTTGTGAGTTCTAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACAC	1966
Db	1076	GTTCCCTACATTGATCAGTTCTAAACTGATTTCATTTTCTAAATTAGCCAGGGAATATAC	1135
Qy	1967	TGACCTAGAAGTAGCCACAAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTCATT	2026
Db	1136	TGACCTAGAAGTATCCACAAAAGTGAAATTGCTAATGCCCCGGATGGAGCTGGGTCATT	1195
Qy	2027	GGCTTGTGCAGGATTGCCCCATGACCTTTCTTTCAAGAGTATACAACCTAAAGAGGAAGT	2086
Db	1196	GCCTTGCACAGAATTGCCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGA	1255
Qy	2087	TCA-----TGTCCCAGATGAGTTCTCCAAAGATAGGGGTGATGTTTCAAAGGTGCCCGT	2140
Db	1256	GAAAATCAGTTTCTCAGATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTT	1315
Qy	2141	ACTGCCTCCAGATGTTTCTGCTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAAACC	2200
Db	1316	ATTGCCTCCAGATGTTTCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACC	1375
Qy	2201	CAAAGTTCTTGTGAAAGAAGCCGAGAGAAAACCTTCCTTCTGATACAGAAAAAGAGCGAAG	2260
Db	1376	CAAAGTTCTTGTGAAAGAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAG	1435
Qy	2261	ATCTCCATCTGCTATATTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTA	2320
Db	1436	ATCACCATCTGCTATATTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTGTA	1495
Qy	2321	CTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTGTTTCCTGCTGCTCTC	2380
Db	1496	CTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTTCCTGCTGCTTTC	1555
Qy	2381	GCTGACAGTATTTCAGCATTGTGAGTGTAAACGGCCTACATTGCCTTGGCCCTGCTCTCTGT	2440

Db	1556		ATTGACAGTATTCAGCATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGT	1615
Qy	2441		GACTATCAGCTTTAGGATATATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGG	2500
Db	1616		GACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGG	1675
Qy	2501		CCACCCATTTCAGGGCATATTTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAA	2560
Db	1676		CCACCCATTTCAGG-----GAAGTTGCTATATCTGAGGAGTTGGTTCAGAA	1720
Qy	2561		GTACAGCAATTCTGCTCTTGGTCATGTTAACTGCACAATAAAAGAACTCAGACGCCTCTT	2620
Db	1721		GTACAGTAATTCTGCTCTTGGTCATGTGAAGTGCACGATAAAGGAACTCAGGCGCCTCTT	1780
Qy	2621		CTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTA	2680
Db	1781		CTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTA	1840
Qy	2681		TGTTGGTGCCTTGTTCAATGGTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAG	2740
Db	1841		TGTTGGTGCCTTGTTTAAATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAG	1900
Qy	2741		TGTTCTCTGTTATTTATGAACGGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAA	2800
Db	1901		TGTTGGTGTATTTATGAACGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAA	1960
Qy	2801		TAAGAATGTTAAAGATGCTATGGCTAAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAA	2860
Db	1961		TAAGAATGTTAAAGATGCTATGGCTAAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAA	2020
Qy	2861		AGCTGAATGAGAAAGCCTGAAAGAGTTAACAATAGAGGAGTTTATCTTTAAAGGGGATAT	2920
Db	2021		AGCTGAATGAAAACGCCCAAATAATTA-----GTAGGAGTTCATCTTTAAAGGGGATAT	2075
Qy	2921		TCATTTGATTCCATTGGGGAGGGTCAGGGAAGAAACAAAGCCTTGACATTGCAGTGCAGTT	2980
Db	2076		TCATTTGATTATACGGGGAGGGTCAGGGAAGAACGAA-CCTTGACGTTGCAGTGCAGTT	2134
Qy	2981		TCAC-----AGATCTTTATTTTGTAGCAACGCAGTG-TCTGAGGAAAAATGACCT	3028
Db	2135		TCACAGATCGTTGTTAGATCTTTATTTTGTAGCCATGCACTGTTGTGAGGAAAAATTACCT	2194
Qy	3029		GTCTTGACTGCCCTGTGTTTCATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTTAAA	3088
Db	2195		GTCTTGACTGCCATGTGTTTCATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTTAAA	2254
Qy	3089		TCGTAATCATATTTGTTTTTCTGTATGAGGCACTGGTGAATAAACAAAGATCTGAGAAA	3148
Db	2255		CCGTAATCATA--TCTTTTTCCTATCTGAGGCACTGGTGGA-----ATAAAAAA	2301
Qy	3149		GCTGTATATTACACTTTGTTCGAGGTAGTCTTGCTGTAT-TTGGGGAATTGCAAAGAAAG	3207
Db	2302		CCTGTATATTTTACTTTGTTGCAGATAGTCTTGCCGCATCTTGGAAGTTGCAGAGATGG	2361
Qy	3208		TGGAGCTGACAGAAATAA 3225	

Qy	1446	TATTCAGAAATAGCAGAAGTTGCACAGCCAGTGCCCGAGCATTCTGAGCTAGTTGAAGAT	1505
Db	148	TATTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCCTGATCATTCTGAGCTAGTTGAAGAT	207
Qy	1506	TCCTCCCCGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCCGAAGTTCCA	1565
Db	208	TCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCTGACGTTCCA	267
Qy	1566	CAAAAACAAGATGAAGCTGTAATACTTGTGAAAAGAAAACCTCACTGAAATTTTCATCTGAG	1625
Db	268	CAAAAACAAGGTGAAACTGTGATGCTTGTGAAAAGAAAGTCTCACTGAGACTTCATTTGAG	327
Qy	1626	TCAATGACAGGACATGACAATAAGGGAAAACTCAGTGCTTCACCATCACCTGAGGGAGGA	1685
Db	328	TCAATGATAGAATATGAAAATAAGGAAAACTCAGTGCTTTTGC---CACCTGAGGGAGGA	384
Qy	1686	AAACCGTATTTGGAGTCTTTTCAGCCCAGTTTAGGCATCACAAAAGATACCTTAGCACCT	1745
Db	385	AAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACCTGTTCACCT	444
Qy	1746	GATGAAGTTTCAGCATTGACCCAAAAGGAGAAAAATCCCTTTGCAGATGGAGGAGCTCAAT	1805
Db	445	GATGAAGTTTCAACATTGAGCAAAAAGGAGAAAAATTCCTTTGCAGATGGAGGAGCTCAGT	504
Qy	1806	ACTGCAGTTTATTCAAGTGATGGCTTATTCATTGCTCAGGAAGCAAACCTAAGAGAAAGT	1865
Db	505	ACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATAAGAGAAACT	564
Qy	1866	GAAACATTTTTCAGATTTCATCTCCGATTGAGATTATAGATGAGTTCCCGACCTTTGTGAGT	1925
Db	565	GAAACGTTTTTCAGATTTCATCTCCAATTGAAATTATAGATGAGTTCCCTACATTGATCAGT	624
Qy	1926	TCTAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACACTGACCTAGAAGTAGCCAC	1985
Db	625	CCTAAAACTGATTCATTTTCTAAATTAGCCAGGGAATATACTGACCTAGAAGTATCCAC	684
Qy	1986	AAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTCAATTGGCTTGTGCAGGATTGCCC	2045
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Qy	2160	GCTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAAACCCAAAGTTCTTGTGAAAGAA	2219
Db	865	GCTTTGGCCACTCAGGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTTGTGAAAGAA	924
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Db	925	GCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCTGCTATATTT	984

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Qy	2340	ACTGGAGTGGTGTGTTGGTGCCAGCTTGTTCTGCTGCTCTCGCTGACAGTATTCAGCATT	2399
Db	1045	ACTGGAGTGGTGTGTTGGTGCCAGCCTATTCCAGCTGCTTTTCATTGACAGTATTCAGCATT	1104
Qy	2400	GTGAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATA	2459
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Qy	2760	CGGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTTAAAGATGCT	2819
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Qy    3166 GTCGCAGGTAGTCTTGCTGTAT-TTGGGGAATTGCAAAGAAAGTGGAGCTGACAGAAATA 3224
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Qy    3225 A 3225
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OM nucleic - nucleic search, using sw model

Run on: January 23, 2004, 02:43:47 ; Search time 194.332 Seconds
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	2687.8	70.1	799	4	US-09-484-970B-106	Sequ 6, Appli
2	590.8	15.4	799	2	US-08-700-607-2	Sequence 2, Appli
3	230.4	6.0	1766	4	US-09-149-476-254	Sequence 254, App
4	230.4	6.0	2664	4	US-09-149-476-255	Sequence 255, App
5	202.2	5.3	1095	2	US-08-700-607-4	Sequence 4, Appli
6	182	4.7	794	4	US-09-149-476-102	Sequence 102, App
7	174.2	4.5	261	2	US-08-700-607-9	Sequence 9, Appli
8	138.6	3.6	301	4	US-09-439-313-279	Sequence 279, App
9	138.6	3.6	301	4	US-09-352-616A-279	Sequence 279, App
10	138.6	3.6	301	4	US-09-232-149A-279	Sequence 279, App
11	113.6	3.0	211	4	US-09-506-729-51	Sequence 51, Appl

c	12	69.4	1.8	7218	1	US-08-232-463-14	Sequence 14, Appl
	13	60.8	1.6	200	3	US-09-221-298-100	Sequence 100, App
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	15	44	1.1	1134	3	US-09-248-335-29	Sequence 29, Appl
c	16	43.8	1.1	1949	4	US-08-961-527-289	Sequence 289, App
	17	43.6	1.1	2439	3	US-09-386-493-1	Sequence 1, Appli
c	18	42.8	1.1	949	3	US-08-714-918-12	Sequence 12, Appl
c	19	42.8	1.1	949	3	US-09-265-315-12	Sequence 12, Appl
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	32	40.8	1.1	3763	1	US-07-792-865D-1	Seq Appli
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	39	39.6	1.0	1342	4	US-09-489-847-89	Sequence 89, Appl
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ALIGNMENTS

RESULT 1

US-09-484-970B-106

; Sequence 106, Application US/09484970B

; Patent No. 6426186

; GENERAL INFORMATION:

; APPLICANT: Jones, Karen A.

; APPLICANT: Volkmuth, Wayne

; APPLICANT: Walker, Michael G.

; TITLE OF INVENTION: BONE REMODELING GENES

; FILE REFERENCE: PB-0014 US

; CURRENT APPLICATION NUMBER: US/09/484,970B

; CURRENT FILING DATE: 2000-01-18

; NUMBER OF SEQ ID NOS: 172

; SOFTWARE: PERL Program

; SEQ ID NO 106

; LENGTH: 4822

; TYPE: DNA

; ORGANISM: Homo sapiens

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 Db 1618 GATCGTTTCAGGAGCATATATCACATGTGCTCCCTTTAACCCAGCAGCAACTGAGAGCATT 1677
 Qy 718 TCAACAAACATTTTTCCCTTTGTTGGAAGATCATACTTCGGAAAATAAGACAGATGAAAAA 777
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Qy	2209	TTGTGAAAGAAGCCGAGAGAAAACTTCCTTCGATACAGAAAAAGAGCGAAGATCTCCAT	2268
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Db 3592 GATGATTTAGTTGATTCTCTGAAGTTTGCAGTGT'TGATGTGGGTATTTACCTATGTTGGT 3651

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Db 3887 ATTATACGGGGAGGGTCAGGGAAGAACGAA-CCTTGACGTTGCAGTGCAGTTTCACAGA 3945

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Db 4006 CTGCCATGTGTTTCATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTTAAACCGTAAT 4065

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Qy 3497 TATGTGTGTAGTCCCAAAGCACATAAGCTAGGGAGAAACGTACTTCTAGGCGCACTACCA 3556
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Qy 3719 GACGATTTATACAATTGTGGTTTAAAGCTGTATTGAACTAAATCTGTGGAATGCATTGTGA 3778
 Db 4702 GAAGATTTATACCATTGTGGTTTAAAGCTGTACTGAACTAAATCTGTGGAATGCATTGTGA 4761

Qy 3779 ACTGTAAAAGCAAAGTATCAATAAAGCTTATAGACTTAAAAAAAAAAAAAAAAAAAA 3833
 Db 4762 ACTGTAAAAGCAAAGTATCAATAAAGCTTATAGACTTAAAANGNNANNAGNGAAA 4816

RESULT 2

US-08-700-607-2

; Sequence 2, Application US/08700607

; Patent No. 5858708

; GENERAL INFORMATION:

; APPLICANT: Bandman, Olga

; APPLICANT: Au-Young, Janice

; APPLICANT: Goli, Surya K.

; APPLICANT: Hillman, Jennifer L.

; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS

; NUMBER OF SEQUENCES: 9

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; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 799 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE: Consensus
US-08-700-607-2

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Query Match          15.4%; Score 590.8; DB 2; Length 799;
Best Local Similarity 92.9%; Pred. No. 9e-139;
Matches 643; Conservative 0; Mismatches 42; Indels 7; Gaps 2;

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Qy      2304 GTTGTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGC 2363
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Db      108 GTTGTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGC 167
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Qy      2364 TTGTTCCCTGCTGCTCTCGCTGACAGTATTTCAGCATTGTGAGTGTAAACGGCCTACATTGCC 2423
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Db      168 CTATTCCCTGCTGCTTTTCATTGACAGTATTTCAGCATTGTGAGCGTAACAGCCTACATTGCC 227
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Qy      2424 TTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAGGCTATC 2483
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Qy      2484 CAGAAATCTGATGAAGGCCACCCATTTCAGGGCATATTTGGAATCTGAAGTTGCTATATCT 2543
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Db      288 CAGAAATCAGATGAAGGCCACCCATTTCAGGGCATATCTGGAATCTGAAGTTGCTATATCT 347
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Qy      2544 GAGGAGTTGGTTTCAGAAGTACAGCAATTCTGCTCTTGGTCATGTAACTGCACAATAAAA 2603
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Db      348 GAGGAGTTGGTTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAAGTGCACGATAAAG 407
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Qy	2604	GAACTCAGACGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTG	2663
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Qy	2664	ATGTGGGTATTTACCTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTAATTTTGGCT	2723
Db	468	ATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAAATGGTCTGACACTACTGATTTTGGCT	527
Qy	2724	CTGATTTCACTCTTCAGTGTTCTGTTATTTATGAACGGCATCAGGCGCAAATAGATCAT	2783
Db	528	CTCATTTCACTCTTCAGTGTTCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT	587
Qy	2784	TATCTGGGACTTGCAAATAAGAAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATC	2843
Db	588	TAT025XA TTGCAAATAAGAAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATC	8423
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Db	648	CCTGGATTGAAGCGCAAAGCTGAATGAAAACGCCCAAATAATTA-----GTAGGAGTTC	702
Qy	2904	ATCTTTAAAGGGGATATTCATTTGATTCCATTGGGGAGGGTCAGGGAAGAACAAGCCTT	2963
Db	703	ATCTTTAAAGGGGATATTCATTTGATTATACGGGGAGGGTCAGGGAAGAACGA--CCTT	760
Qy	2964	GACATTGCAGTGCAGTTTCACAGATCTTTATT	2995
Db	761	GACGTTGCAGTGCAGTTTCACAGATCGTTGTT	792

RESULT 3

US-09-149-476-254

; Sequence 254, Application US/09149476

; Patent No. 6420526

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: 186 Human Secreted proteins

; FILE REFERENCE: PZX6 P1

9

; CURRENT APPLICATION NUMBER: US/09/149,476

; CURRENT FILING DATE: 1998-09-08

; EARLIER APPLICATION NUMBER: PCT/US98/04493

; EARLIER FILING DATE: 1998-03-06

; EARLIER APPLICATION NUMBER: 60/040,162

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/040,333

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; EARLIER APPLICATION NUMBER: 60/038,621

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/040,626

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/040,334

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; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05

; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

Query Match 6.0%; Score 230.4; DB 4; Length 1766;
Best Local Similarity 63.6%; Pred. No. 3.8e-48;
Matches 351; Conservative 0; Mismatches 201; Indels 0; Gaps 0;

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Db      286  TCGGGTGCACGATCTGATTTTCTGGAGAGATGTGAAGAAGACTGGGTTTGTCTTTGGCAC 345

Qy      2360 CAGCTTGTTCCCTGCTGCTCTCGCTGACAGTATTTCAGCATTGTGAGTGTAAACGGCCTACAT 2419
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Db      346  CACGCTGATCATGCTGCTTTCCCTGGCAGCTTTCAGTGTTCATCAGTGTGGTTTCTTACCT 405

Qy      2420 TGCCTTGGCCCTGCTCTCTGTGACTATC1 TAGGATATATAAGGGTGTGATCCAGGC 2476
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Db      406  CATCCTGGCTCTTCTCTCTGTCCCATCAGCTTCAGGATCTACAAGTCCGTCATCCAAGC 465

Qy      2480 TATCCAGAAATCTGATGAAGGCCACCCATTCAGGGCATATTTGGAATCTGAAGTTGCTAT 2539
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Qy      2540 ATCTGAGGAGTTGGTTTCAGAAGTACAGCAATTCTGCTCTTGGTCATGTTAACTGCACAAT 2599
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Qy      2600 AAAAGAACTCAGACGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGT 2659
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Qy      2840 AATCCCTGGATT 2851
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RESULT 4

US-09-149-476-255

; Sequence 255, Application US/09149476

; Patent No. 6420526

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: 186 Human Secreted proteins

; FILE REFERENCE: PZ002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
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; EARLIER FILING DATE: 1997-05-23
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CG9CCA 2150 50XT

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; EARLIER APPLICATION NUMBER: 60/056,845
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; EARLIER APPLICATION NUMBER: 60/056,892
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,76
; EARLIER FILING DATE: 1997-08-22
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; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997 04-11
; EARLIER APPLICATION NUMBER: 60/043,576
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; EARLIER APPLICATION NUMBER: 60/056,881
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 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/057,650
 ; EARLIER FILING DATE: 1997-09-05
 ; EARLIER APPLICATION NUMBER: 60/056,884
 ; EARLIER FILING DATE: 1997-08-22
 ; EARLIER APPLICATION NUMBER: 60/057,669
 ; EARLIER FILING DATE: 1997-09-05
 ; EARLIER APPLICATION NUMBER: 60/049,610
 ; EARLIER FILING DATE: 1997-06-13
 ; EARLIER APPLICATION NUMBER: 60/061,060
 ; EARLIER FILING DATE: 1997-10-02

Query Match 6.0%; Score 230.4; DB 4; Length 2664;
 Best Local Similarity 63.6%; Pred. No. 4.6e-48;
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Qy 2300 TTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGC 2359
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 Db 261 TGCGGTGCACGATCTGATTTTCTGGAGAGATGTGAAGAAGACTGGGTTTGTCTTTGGCAC 320
 Qy 2360 CAGCTTGTTCTCTGCTCTCGCTGACAGTATTTCAGCATTGTGAGTGTAAACGGCCTACAT 2419
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 Db 321 CACGCTGATCATGTCTGCTTTCCCTGGCAGCTTTTCAGTGTTCATCAGTGTGGTTTCTTACCT 380
 Qy 2420 TGCCTTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAGGC 2479
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 Db 381 CATCCTGGCTCTTCTCTCTGTCAACCATCAGCTTCAGGATCTACAAGTCCGTCATCCAAGC 440
 Qy 2480 TATCCAGAAATCTGATGAAGGCCACCCATTTCAGGGCATATTTGGAATCTGAAGTTGCTAT 2539
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 Db 441 TGTACAGAAGTCAGAAGAAGGCCATCCATTCAAAGCCTACCTGGACGTAGACATTACTCT 500
 Qy 2540 ATCTGAGGAGTTGGTTTCAAGAAGTACAGCAATTCTGCTCTTGGTCATGTTAACTGCACAAAT 2599
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 Db 501 GTCCTCAGAAGCTTCCATAATTACATGAATGCTGCCATGGTGCACATCAACAGGGCCCT 560
 Qy 2600 AAAAGAACTCAGACGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGT 2659
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 Db 561 GAAACTCATTATTTCGTCTCTTTCTGGTAGAAGATCTGGTTGACTCCTTGAAGCTGGCTGT 620
 Qy 2660 GTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTCATGGTCTGACACTACTAATTTT 2719
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 Db 621 CTTGATGTGGCTGATGACCTATGTTGGTGTGTTTTTAACGGAATCACCCCTTCTAATTCT 680

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Qy      2720 GGCTCTGATTTCACTCTTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCGCAAATAGA 2779
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Db      681 TGCTGAAGTCTCATTTTCAGTGTCCCGATTGTCTATGAGAAGTACAAGACCCAGATTGA 740

Qy      2780 TCATTATCTGGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAA 2839
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Db      741 TCACTATGTTGGCATCGCCCGAGATCAGACCAAGTCAATTGTTGAAAAGATCCAAGCAAA 800

Qy      2840 AATCCCTGGATT 2851
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Db      801 ACTCCCTGGAAT 812

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RESULT 5

US-08-700-607-4

; Sequence 4, Application US/08700607

; Patent No. 5858708

; GENERAL INFORMATION:

; APPLICANT: Bandman, Olga

; APPLICANT: Au-Young, Janice

; APPLICANT: Goli, Surya K.

; APPLICANT: Hillman, Jennifer L.

; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: U.S.

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ Version 1.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/700,607

; FILING DATE: Filed Herewith

; ATTORNEY/AGENT INFORMATION:

; NAME: Billings, Lucy J.

; REGISTRATION NUMBER: 36,749

; REFERENCE/DOCKET NUMBER: PF-0114 US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-855-0555

; TELEFAX: 415-845-4166

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1095 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; IMMEDIATE SOURCE:

; LIBRARY: THP1NOB01

; CLONE: 31870

US-08-700-607-4

Query Match 5.3%; Score 202.2; DB 2; Length 1095;
Best Local Similarity 63.7%; Pred. No. 3.7e-41;
Matches 303; Conservative 1; Mismatches 172; Indels 0; Gaps 0;

Qy 2300 TTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGC 2359
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Db 328 TGCGGTGCACGATCTGATTTTMTGGAGAGATGTGAAGAAGACTGGGTTTGTCTTTGGCAC 387

QY 2360 CAGCTTGTTCCTGCTGCTCTCGCTGACAGTATTAGCATTGTGAGTGTAAACGGCCTACAT 2419
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Db 388 CACGCTGATCATGCTGCTTTCCCTGGCAGCTTTCAGTGTATCAGTGTGGTTTCTTACCT 447

Qy 2420 TGCCTTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAGGC 2479
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T Db 448 CATCCTGGCTCTTCTCTCTGTCAACCATCAGCTTC AGTCCGTCATGCACAT 5089

QY 2480 TATCCAGAAATCTGATGAAGGCCACCCATTAGGGCATATTTGGAATCTGAAGTTGCTAT 2539
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Db 508 TGTACAGAAGTCAGAAGAAGGCCATCCATTCAAAGCCTACCTGGACGTAGACATTACTCT 567

Qy 2540 ATCTGAGGAGTTGGTTCAGAAGTACAGCAATTCTGCTCTTGGTCATGTTAACTGCACAAT 2599
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Db 568 GTCCTCAGAAGCTTTCATAATTACATGAATGCTGCCATGGTGCACATCAACAGGGCCCT 627

Qy 2600 AAAAGAACTCAGACGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGT 2659
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Db 628 GAAACTCATTATTCTGCTCTTTCTGGTAGAAGATCTGGTTGACTCCTTGAAGCTGGCTGT 687

Qy 2660 GTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTAATTTT 2719
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A Db 688 CTTCATG CTATGTTGGTGTCTGTTTTTAACGGAATCACCCCTTCTATTTCT 3484

Qy 2720 GGCTCTGATTTCACTCTTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCGCAAA 2775
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RESULT 6
US-09-149-476-102
; Sequence 102, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: PZ002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
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; EARLIER FILING DATE: 1997-08-22

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; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02
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Query Match          4.7%; Score 182; DB 4; Length 794;
Best Local Similarity 61.2%; Pred. No. 3.7e-36;
Matches 333; Conservative 6; Mismatches 201; Indels 4; Gaps 3;
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Db      253 TGCCTGACCTGCTGATTTTCTGGAGAXo GAAGAAGACTGGGTTTGTCTTTG--GA 310

Qy      2360 CAGCTTGTTCTGCTGCTCTCGCTGACAGTATTCAGCATTGTGAGTGTAACGGCC-TACA 2418
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Db      311 CACGCTGATCATGCTGCTTTCCCTGGCAGCTTTCAGTGTGCATCARTGTGGGTTTCTTAMC 370

Qy      2419 TTGCCTTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAGG 2478
          || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      371 TCATCCTGGCTCTTCTCTGTCAACCATCARCTTCAGGATCTACAAGTCCGTCATCCAAG 430

Qy      2479 CTATCCAGAAATCTGATGAAGGCCACCCATT-CAGGGCATATTTGGAATCTGAAGTTGCT 2537
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Db      431 CTGTWCAGAARTCAGAARAAGGCCATCCAWTCCAAAGCCTACCTGGACGTAGACATTACT 490

Qy      2538 ATATCTGAGGAGTTGGTTTCAGAAGTACAGCAATTCTGCTCTTGGTCATGTTAACTGCACA 2597
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Db      x2 1 CTGTCCTCAGAAGCTTTCCATAATTACATGAATGCTGCCATGGTGCACATCAACAGGGCC 550

Qy      2598 ATAAAAGAACTCAGACGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCA 2657
          || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      551 CTGAAACTCATTATTTCGTCTCTTTCTGGTAGAAGATCTGGTTGACTCCTTGAAGCTGGCT 610

Qy      2658 GTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTCATGGTCTGACACTACTAATT 2717
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Db      611 GTCTTCATGTGGCTGATGACCTATGTTGGTGTCTGTTTTTAACGGAATCACCCCTTCTAATT 670

Qy      2718 TTGGCTCTGATTTCACTCTTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCGCAAATA 2777
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Db      671 CTTGCTGAACTGCTCATTTTTCAGTGTCCCGATTGTCTATGAGAAGTACAAGACCCAGATT 730

Qy      2778 GATCATTATCTGGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCA 2837
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Db      731 GATCACTATGTTGGCATCGCCCGAGATCAGACCAAGTCAATTGTTGAAAAGATCCCAAGC 790

Qy      2838 AAAA 2841
          |||||
Db      791 AAAA 794
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US-08-700-607-9

US-08-700-607-9

Qy | 2363 CTTGTTCTCTGCTGCTCTCGCTGACAGTATTTCAGCATTGTGAGTGTAACGGCCTACATTGC 2422
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Db 1 CCTATNCCNGCTGCTTTTCATTGACAGTATTTCAGCATTGTGAGCGTAACAGCCTACATTGC 60

Qy | 3 CTTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATTCAGGCTAT 2482
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Db 61 CTTNGCCCTGCNCCTCTGTGACCATCAGCTNTAGGCTATACAAGGGTGTGATCCAAGCTAT 120


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Db      114 ACAAAGCTTAGACCTTTACCTT-CCAGCCACCCACAGTGCCTTGATATTTTCAGAGTCAGT 172
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Db      173 CATTGGTTATACATGTGTAGTTCCAAAGCACATAAGCTAGAAANAANAATATTTCTAGGG 232
Qy      3547 CGCACTACCATCTGTTTTTCAACACGAACCGACGCCATGCAAAACAGAACTCCTCAACATAA 3606
      ||||||||||||||||| | | ||| || | ||||||| ||||| |
Db      233 AGCACTACCATCTGTTTTTCA---CATGAAATGCCACACACATAGAACTC--CAACATCA 286
Qy      3607 ACTTCACTGCACAGA 3621
      | ||| |||||||
Db      287 ATTTCA TTGCACAGA 301

```

RESULT 9

US-09-352-616A-279

; Sequence 279, Application US/09352616A

; Patent No. 6395278

; GENERAL INFORMATION:

; APPLICANT: Dillon, Davin C.

```
; APPLICANT: Harlocker, Susan Louise
```

; APPLICANT: Jiang, 750Xi

; APPLICANT: Xu, Jiangchun

; APPLICANT: Mitcham, Jennifer Lynn

TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS

TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE

FILE REFERENCE: 210121.427C8

```

; CURRENT APPLICATION NUMBER: US/09/3521616A|||||||atxia805Xe

```

CURRENT FILING DATE: 1999-07-13

; NUMBER OF SEQ ID NOS: 472

```

; SOFTWARE:  FastSEQ for Windows Version 3.0

```

; SEO ID NO 279

```

; LENGTH: 301

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TYPE: DNA

; ORGANISM: Homo sapien

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; FEATURE:

```

```
; NAME/KEY: misc feature
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```

; LOCATION: (1)...(301)

```

OTHER INFORMATION: n = A,T,C or G

US-09-352-616A-279

Query Match 3.6%; Score 138.6; DB 4; Length 301;

Best Local Similarity 80.3%; Pred. No. 1.9e-25;

Matches 253; Conservative 0; Mismatches 41; Indels 21; Gaps 7;

Qy 3314 AAGGCAGGAGTGAAAAAGCTTGCCTTTCCTGGTATGTTCTAGGTGTATTGTGAAATTTAC 3373
 || |||||
 Db 1 AAAGCAGGAATGACAAAGCTTG-CTTTTCTGGTATGTTCTAGGTGTATTGTGACTTTTAC 59

[illegible]

QY 3434 ACGAAGCTTAGCCCTTTACCTTCCCAGCTGCCCCACAGTGCTTGATACT-----TCTGT 3487
|| ||||||| ||||||||| |||| | ||||||||| ||||| ||
Db 114 ACAAGCTTAGACCTTTACCTT-CCAGCCACCCAAGTGCTTGATATTTCAGAGTCAGT 172

```

Qy      3488 CATGGGTTTTATGTGTGTAGTCCCAAAGCACATAAGCTAGGGAGAAAACGTACTTCTA-GG 3546
          ||| ||| | | ||||| | | | | | | | | | | | | | | | | | | | | | | | |
Db      173 CATTGGTTATACATGTGTAGTTCCAAAGCACATAAGCTAGAANAANAATATTCTAGGG 232

Qy      3547 CGCACTACCATCTGTTTTCAACACGAACCGACGCCATGCAAACAGAACTCCTCAACATAA 3606
          ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      233 AGCACTACCATCTGTTTTCA---CATGAAATGCCACACACATAGAAGTC--CAACATCA 286

Qy      3607 ACTTCACTGCACAGA 3621
          | ||| | | | | | |
Db      287 ATTTCACTGCACAGA 301

```

US-09-232-149A-279

; Patent No. 6465611

; APPLICANT: Xu, Jian

; APPLICANT: Mitcham, Jennife

TITLE OF INVENTION: COMPOUNDS FOR

TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE

FILE REFERENCE: 210121.427C6

; CURRENT APPLICATION NUMBER:

; CURRENT FILING DATE: 1999-01-15

```
;  NUMBER OF SEQ ID NOS: 338
```

; SOFTWARE: FastSEQ for Win

; SEQ ID NO 279

```
; LENGTH: 301
```

; TYPE: DNA

; ORGANISM:

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; FEATURE:
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```
; NAME/KEY
```

; LOCATION: (1) ... (301)

; OTHER INFORMATION: n

US-09-232-149A-279

Query Match 3.6%; Score 138.6; DB 4; Length 301;

Best Local Similarity 80.3%; Pred. No. 1.9e-25;

Matches 253; Conservative 0; Mismatches 41; Indels 21; Gaps 7;

Qy 3314 AAGGCAGGAGTGAAAAAGCTTGCCTTTCTCGGTATGTTCTAGGTGTATTGTGAAATTTAC 3373
 || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 AAAGCAGGAATGACAAAGCTTG-CTTTTCTGGTATGTTCTAGGTGTATTGTGACTTTTAC 59

Qy 3434 ACGAAGCTTAGCCCTTTACCTTCCCAGCTGCCCCACAGTGCTTGATACT-----TCTGT 3487
 ||||||| ||||||| ||||| ||||||| ||||| |||||
 Db 114 ACAAAGCTTAGACCTTTACCTT-CCAGCCACCCACAGTGCTTGATATTTAGAGTCAGT 172

```

Db      173 CATTGGTTATACATGTGTAGTTCCAAAGCACATAAGCTAGAANAANAATATTTCTAGGG 232

Qy      3547 CGCACTACCATCTGTTTTCAACACGAACCGACGCCATGCAAACAGAACTCCTCAACATAA 3606
          |||||||||||||||| | ||| | | |||||| | ||||| |
Db      233 AGCACTACCATCTGTTTTCA----CATGAAATGCCACACACATAGAAGTC--CAACATCA 286

Qy      3607 ACTTCACTGCACAGA 3621
          | ||| | |||||
Db      287 ATTTCACTGCACAGA 301

```

RESULT 11

US-09-506-729-51

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; Sequence 51, Application US/09506729
; Patent No. 6365352
; GENERAL INFORMATION:
; APPLICANT: Yerramilli, Subrahmanyam V.
; APPLICANT: Prashar, Yatindra
; APPLICANT: Newberger, Peter
; APPLICANT: Goguen, Jon
; APPLICANT: Weissman, Sherman M.
; TITLE OF INVENTION: A PROCESS TO STUDY CHANGES IN GENE EXPRESSION IN
; TITLE OF INVENTION: GRANULOCYTIC CELLS
; FILE REFERENCE: 44921-5016-US
; CURRENT APPLICATION NUMBER: US/09/506,729
; CURRENT FILING DATE: 2000-02-18
; EARLIER APPLICATION NUMBER: PCT/US98/17284
; EARLIER FILING DATE: 1998-08-21
; EARLIER APPLICATION NUMBER: 60/056,844
; EARLIER FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 51
; LENGTH: 211
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-506-729-51

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```

Query Match          3.0%; Score 113.6; DB 4; Length 211;
Best Local Similarity 78.0%; Pred. No. 3e-19;
Matches 167; Conservative 0; Mismatches 34; Indels 13; Gaps 2;

```

```

Qy      2986 GATCTTTATTTTGTAGCAACGCAGTGTCTGAGGAAAAATGACCTGTCTTGACTGCCCTGTG 3045
          |||||||||||||||| | ||| | | |||||| | ||||| |
Db      1 GATCTTTATTTTGTAGCCATGCACTGTTGTGAGGAAAATTACCTGTCTTGACTGCCATGTG 60

Qy      3046 TTCATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTAAATCGTAATCATATTTGTT 3105
          *p77$Xt$ |||||||||||||||||||||||||||||||||| |||
Db      61 TTCATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTAAACCGTAATCATATCTTTT 120

Qy      3106 T--TTCCTGTATGAGGCACTGGTGAATAAACAAAGATCTGAGAAAGCTGTATATTACACT 3163
          | | || | |||||||||||| | | | ||||||| |||
Db      121 TCCTATCTATCTGAGGCACTGGTGGA-----ATAAAGAACCTGTATATTTTACT 169

Qy      3164 TTGTCGCAGGTAGTCTTGCTGTATTTGGGGAATT 3197
          |||| |||| |||||||| | || | || ||
Db      170 TTGTTGCAGATAGTCTTGCCGCATCTTGGCAAGT 203

```


US-08-232-463-14/c

; Patent No. 5670367

APPLICANT: DORNER, F.

APPLICANT: FALKNER, F. G.

```

: NUMBER OF SEQUENCES: 52

```

ADDRESSEE: Foley & Lardner

;
CITY: Alexandria

```

, STATE: VA
; COUNTRY: USA

```

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

```

;      OPERATING SYSTEM:  PC DOS/MS DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25

```

APPLICATION NUMBER: US/08/232,463

CLASSIFICATION: 435

APPLICATION NUMBER: US/07/93

APPLICATION NUMBER: EP 91 114 300.6

ATTORNEY/AGENT INFORMATION:

NAME: BENT, Stephen A.

REFERENCE/DOCKET NUMBER: 30472/114 IMMU

TELEPHONE: (703) 836-9300

TELEX: 899149

; SEQUENCE CHARACTERISTICS:

```

; TYPE: nucleic acid

```

```

; TOPOLOGY: linear

```

CLONE: pTZqpt-F1s

Query Match 1.8%; Score 69.4; DB 1; Length 7218;

Best Local Similarity 4.1%; Pred. No. 1.9e-07;

Matches 16; Conservative 233; Mismatches 144; Indels 0; Gaps 0;

Qv 234 AGTAGCGAATCCTAGGGACGAAATAGTTGTGAGGAGTAGAGATAAAGAAGAGGACTTAGT 293

[illegible]

```

Db      1464 AGTAGTTAAAGAGATAGAAGAATTTGGTACRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1405
Qy      294 TAGTCTTAACATCCTTCATACTCAGCAGGAGTTATCTACAGTCCTTACGAAATCAGTTGA 353
      :: :: : : : : : : : : : : : : : : : : : :
Db      1404 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1345
Qy      354 AGAAGAAGATAGAGTTCTGTCTCCAGAAAAACAAAGGACAGTTTAAAGGAAAAGGGAGT 413
      :::::::::: : : : : : : : : : : : : : : : : : :
Db      1344 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1285
Qy      414 TGCAGCAGAAGCTTCTATGGGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATG 473
      : : : : : : : : : : : : : : : : : : : : : : : :
Db      1284 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1225
Qy      474 GGAAGTGAAAGATACTTACAAGCAAGATAGTGATGTTTTGATTGCTGGAGGTAATATAGA 533
      7 TTCTCTAGTT:: : : : : : : : : : : : : : : : : :
Db      1224 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1165
Qy      534 GAGCAAATTGGAAGGTAAAGTGGATAAGAAACACTTTTCAGATAGCCTTGAACAAACAAA 593
      :: : : : : : : : : : : : : : : : : : : : : : :
Db      1164 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1105
Qy      594 TCGTGAAAAAGATAGTGAAAGCAGTAATGATGA 626
      : : : : : : : : : : : : : : : : : : : :
Db      1104 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1072

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RESULT 13

US-09-221-298-100

; Sequence 100, Application US/09221298

; Patent No. 6284241

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY AND DIAGNOSIS

; TITLE OF INVENTION: OF COLON CANCER

; FILE REFERENCE: 210121.471

; CURRENT APPLICATION NUMBER: US/09/221,298

; CURRENT FILING DATE: 1998-12-23

; N| SEQ ID NOS: 112

|||| ||0

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 100

; LENGTH: 200

; TYPE: DNA

; ORGANISM: Human

; FEATURE:

; NAME/KEY: modified_base

; LOCATION: (3)

; OTHER INFORMATION: Where n is a, c, g or t

; FEATURE:

; NAME/KEY: modified_base

; LOCATION: (5)

; OTHER INFORMATION: Where n is a, c, g or t

; FEATURE:

; NAME/KEY: modified_base

; LOCATION: (6)

; OTHER INFORMATION: Where n is a, c, g or t

; FEATURE:

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; NAME/KEY: modified_base
; LOCATION: (14)
; OTHER INFORMATION: Where n is a, c, g or t
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (21)
; OTHER INFORMATION: Where n is a, c, g or t
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (23)
; OTHER INFORMATION: Where n is a, c, g or t
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (29)
; OTHER INFORMATION: Where n is a, c, g or t
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (46)
; OTHER INFORMATION: Where n is a, c, g or t
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (71)
; OTHER INFORMATION: Where n is a, c, g or t
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (150)
; OTHER INFORMATION: Where n is a, c, g or t
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (151)
; OTHER INFORMATION: Where n is a, c, g or t
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (166)
; OTHER INFORMATION: Where n is a, c, g or t
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (176)
; OTHER INFORMATION: Where n is a, c, g or t
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (185)
; OTHER INFORMATION: Where n is a, c, g or t
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (186)
; OTHER INFORMATION: Where n is a, c, g or t
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (195)
; OTHER INFORMATION: Where n is a, c, g or t
US-09-221-298-100

```

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Query Match          1.6%;  Score 60.8;  DB 3;  Length 200;
Best Local Similarity 66.5%;  Pred. No. 5.2e-06;
Matches 111;  Conservative 0;  Mismatches 48;  Indels 8;  Gaps 2;

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Qy 3517 ACATAAGCTAGGGAGAAACGTA^TCTTAGCGCACTACCATCTGT^TTTTCAACACGAACCG 3576
Db 1 ACNTNNACTAGAANTAACAGNCN^TTTCTANGAACACTACCATCTGT^NTTTCATGAAATGC 60

Qy 3577 ACGCCATGCAAACAGAACTCCTCAACATAA^ACTTCACTGCACAGACTTACTGTAGTTAAT 3636
Db 61 CACACACATANAAA-----CTCCAACATCAAT^TTTCAATTGCACAGACTGACTGTAA^TTTAAT 115

Qy 3637 TTTATCAC---AAACTCTGGACTGAATCTAATGCTTCCAAAAATGTT 3680
Db 116 TTTGTACAGGAATCTATGGACTGAATCTAATGCN^NCCCCAAATGTT 162

```

Query Match          1.2%;   Score 46.6;   DB 6;   Length 1464;   1464
Best Local Similarity 47.2%;   Pred. No. 0.067;
Matches 142;   Conservative 0;   Mismatches 159;   Indels 0;   Gaps 0;

Qy      1285 ATGTATCACTAAAAAAGAATCAGGAATGAATGAAGAAATCACAGAGCCTGAAGGTATTA 1344
          | | ||| | | | | | | | | | | | | | | | | | | | |
Db      359 AAGAATCAGGTGAAAGTGGATTAGTTGATAATGAAGAAGGTGATTTTGAAGACCTAATC 418

Qy      1345 GTGTAGCTGTTTCAGGAAACAGAAGCTCCTTATATATCTATTGCATGTGATTTAATTAAAG 1404
          | | | | | | | | | | | | | | | | | | | | | | | |
Db      419 ATGAAGAATTTGAACCTGATCAAAATGACTCTGAATTAAGTGAAGTGAATTTAGTTGAAT 478

Qy      1405 AAACAAAGATCTCTACTGAACCGACTCCAGATTTCTCTAGTT
          | | | | | | | | | | | | | | | | | | | | | | | |
Db      479 CAGAAAAAAGTGTATCTGAACCAGCTGAACATGTAGAAATTGTATCAGAAAAAAGTGTAT 538

Qy      1465 TTGCACAGCCAGTGCCCCGAGCATTCTGAGCTAGTTGAAGATTCCCTCCCCGATTCTGAAC 1524
          | | | | | | | | | | | | | | | | | | | | | | | |
Db      539 CTGAACCAGCTGAACACGTAGAAATTGTATCTGAAAAAAGTACATCCGAACCAGCTGAAC 598

Qy      1525 CAGTTGACTTATTTAGTGATGATTCAATACCCGAAGTTCCACAAAAACAAGATGAAGCTG 1584
          | | | | | | | | | | | | | | | | | | | | | | | |
Db      599 ATGTAGAAAAGTGTATCTGAACAAAGTAATAACGAACCATCCGAAAAGAAAGATGGACCAG 658

Qy      1585 T 1585
          |
Db      659 T 659

```

US-09-248-335-29

; Sequence 29, Application US/09248335
; Patent No. 6096504
; GENERAL INFORMATION:
; APPLICANT: MCGONIGLE, BRIAN
; APPLICANT: O'KEEF, DANIEL
; TITLE OF INVENTION: PLANT GLUTATHIONE-S-TRANSFERASE ENZYMES
; FILE REFERENCE: CL-1128-A
; CURRENT APPLICATION NUMBER: US/09/248,335
; CURRENT FILING DATE: 1999-02-10
; EARLIER APPLICATION NUMBER: 08/924,759
; EARLIER FILING DATE: 1997-September-05
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Microsoft Word Version 7.0A
; SEQ ID NO 29
; LENGTH: 1134
; TYPE: DNA
; ORGANISM: maize
US-09-248-335-29

Query Match 1.1%; Score 44; DB 3; Length 1134;
Best Local Similarity 61.2%; Pred. No. 0.19;
Matches 71; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

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Qy      3718 TGACGATTATACAATTGTGGTTTAAAGCTGTATTGAACTAAATCTGTGGAATGCATTGTG 3777
          ||  |||| |  ||||| | || | |||| | | | || || || | ||
Db      971 TGGGTATTTGTTGTATTGTGATGTACGGAGTATTCATCAACTCCTTTTGCAAGATTGGTC 1030

Qy      3778 AACTGTAAAAGCAAAGTATCAATAAAGCTTATAGACTTAAAAAAAAAAAAAAAAAAAA 3833
          || | | | |||| | || || | | | ||||| ||||| |||||
Db     1031 AATTATTCAGGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1086
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Search completed: January 23, 2004, 15:31:22
Job time : 196.332 secs

OM nucleic - nucleic search, using sw model

Run on: January 23, 2004, 02:28:33 ; Search time 1153.34 Seconds
(without alignments)
11885.997 Million cell updates/sec

Title: US-09-830-972-28
Perfect score: 3833
Sequence: 1 ctatctcctctctcagccgc.....ttaaaaaaaaaaaaaaaaaaaaaa 3833

Scoring table: IDENTITY ~~NECXA~~ /2/pubpna/US10A_PUBCOMB.seq:* AC TCA 1545
Gapop 10.0 , Gapext 1.0

Searched: 2356869 seqs, 1788235258 residues

Total number of hits satisfying chosen parameters: 4713738

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

5 Listing first 45 mmaries AG

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq2:*
14: /cg
15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query					
No.	Score	Match	Length	DB	ID		Description

1	2649.8	69.1	4632	15	US-10-060-036-53	Sequence 53, Appl
2	2379.4	62.1	4053	9	US-09-758-140-5	Sequence 5, Appli
3	2379.4	62.1	4053	9	US-09-972-599A-5	Sequence 5, Appli
4	2223.6	58.0	3579	9	US-09-789-386-1	Sequence 1, Appli
5	2223.6	58.0	3579	9	US-09-893-348-22	Sequence 22, Appl
6	2179.4	56.9	4684	9	US-09-893-348-17	Sequence 17, Appl
7	1414.6	36.9	1980	13	US-10-220-891-22	Sequence 22, Appl
8	1025.4	26.8	2235	15	US-10-060-036-54	Sequence 54, Appl
9	915.6	23.9	1785	12	US-10-439-388-62	Sequence 62, Appl
10	826.4	21.6	2782	13	US-10-205-194-165	Sequence 165, App
11	685.8	17.9	1610	9	US-09-765-205-5	Sequence 5, Appli
12	683	17.8	1160	15	US-10-175-523-156	Sequence 156, App
13	538.8	14.1	868	9	US-09-789-386-3	Sequence 3, Appli
c 14	535	14.0	4710	11	US-09-764-891-7385	Sequence 7385, Ap
15	527	13.7	1122	9	US-09-789-386-5	Sequence 5, Appli
16	484.6	12.6	972	13	US-10-437-931-1	Sequence 1, Appli
17	464	12.1	472	10	US-09-983-965-507	Sequence 507, App
18	443.4	11.6	459	14	US-10-079-623-238	Sequence 238, App
19	427.2	11.1	447	10	US-09-983-965-190	Sequence 190, App
20	427	11.1	441	10	US-09-983-965-3801	Sequence 3801, Ap
21	423.8	11.1	429	10	US-09-983-965-2991	Sequence 2991, Ap
22	422	11.0	422	10	US-09-960-352-8477	Sequence 8477, Ap
23	418.8	10.9	422	10	US-09-960-352-11567	Sequence 11567, A
24	398	10.4	406	10	US-09-983-965-293	Sequence 293, App
25	383.4	10.0	423	10	US-09-960-352-9092	Sequence 9092, Ap
26	354.4	9.2	389	10	US-09-960-352-5154	Sequence 5154, Ap
27	352.2	9.2	357	10	US-09-983-965-2974	Sequence 2974, Ap
28	337.4	8.8	3413	14	US-10-001-843-61	Sequence 61, Appl
c 29	316.6	8.3	3413	14	US-10-001-843-61	Sequence 61, Appl
30	300.4	7.8	302	10	US-09-983-965-72	Sequence 72, Appl
31	277.6	7.2	668	12	US-10-264-237-163	Sequence 163, App
32	270	7.0	431	10	US-09-960-352-2205	Sequence 2205, Ap
33	267.6	7.0	1520	15	US-10-084-817-333	Sequence 333, App
34	266.8	7.0	3202	10	US-09-954-456-210	Sequence 210, App
35	255.8	6.7	262	14	US-10-079-623-283	Sequence 283, App
36	254.4	6.6	1502	13	US-10-205-219-94	Sequence 94, Appl
37	251	6.5	263	10	US-09-983-965-5543	Sequence 5543, Ap
38	250.4	6.5	1473	13	US-10-205-194-128	Sequence 128, App
39	233.8	6.1	330	14	US-10-040-739-366	Sequence 366, App
40	231.8	6.0	3637	12	US-10-108-260A-449	Sequence 449, App
41	231.8	6.0	363		-10-159-563-443	Sequence 443, App
42	230.4	6.0	1330	15	US-10-106-698-1945	Sequence 1945, Ap
43	230.4	6.0	1656	9	US-09-729-674-19	Sequence 19, Appl
44	230.4	6.0	1668	9	US-09-765-205-25	Sequence 25, Appl
45	230.4	6.0	1766	11	US-09-809-391-254	Sequence 254, App

ALIGNMENTS

RESULT 1

US-10-060-036-53

; Sequence 53, Application US/10060036

; Publication No. US20030073144A1

; GENERAL INFORMATION:

; APPLICANT: Benson, Darin R.

```

; APPLICANT: Kalos, Michael D.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Persing, David H.
; APPLICANT: Hepler, William T.
; APPLICANT: Jiang, Yuqiu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
; FILE REFERENCE: 210121.566
; CURRENT APPLICATION NUMBER: US/10/060,036
; CURRENT FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 4560
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 4632
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-036-53

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Query Match 69.1%; Score 2649.8; DB 15; Length 4632;
Best Local Similarity 85.0%; Pred. No. 0;
Matches 3292; Conservative 0; Mismatches 442; Indels 137; Gaps 24;

Qy	1	CTATCTCCTCTCTCAGCCGCTGCTTTTAAAGAACGTGAATACCTTGGTGATTTACCAGCA	60
Db	853	CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAATTTGTCAACA	912
Qy	61	GTACTGCCCACTGAAGGAACACTTCCAGCAACTTCAAATGAAGCTTCTAAAGCATTTCTCA	120
Db	913	GTATTACCCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA	972
Qy	121	GAGAAGGCAAAAAATCCATTTGTAGAGAGAAATTTAACAGAATTTTCAGAAATTGGAATAT	180
Db	973	GAGAAGGCAAAACTCTACTCATAGATAGAGATTTAACAGAGTTTTCAGAAATTAGAATAC	1032
Qy	181	TCAGAAATGGAATCATCATTCACTGAGTGGCTCTCAAAGGCAGAACCTGCCGTAACAGTAGCG	240
Db	1033	TCAGAAATGGGATCATCGTTCACTGAGTGGCTCTCAAAGGCAGAACCTGCCGTAATAGTAGCA	1092
Qy	241	AATCCTAGGGACGAAATAGTTGTGAGGAGTAGAGATAAAGAAGAGGACTTAGTTAGTCTT	300
Db	1093	AATCCTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGTTAGTTAGTAAT	1152
Qy	301	AACATCCTTCATACTCAGCAGGAGTTATCTACAGTCCTTACGAAATCAGTTGAAGAAGAA	360
Db	1153	AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT	1212
Qy	361	GATAGAGTTCTGTCTCCAGAAAAAACAAGGACAGTTTTAAGGAAAAGGGAGTTGCAGCA	420
Db	1213	GA---AGTTGTGTCTTCAGAAAAAGCAAAAGACAGTTTTAATGAAAAGAGAGTTGCAGTG	1269
Qy	421	GAAGCTTCTATGGGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG	480
Db	1270	GAAGCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG	1329
Qy	481	AAAGATACTTACAAGCAAGATAGTGATGTTTTGATTGCTGGAGGTA	540
Db	1330	AAAGATAGT---AAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAAAATCGAGAGCAAC	1386

5XC

Qy	541	TTGGAAGGTAAAGTGGATAAGAAACACTTTTCAGATAGCCTTGAACAAACAAATCGTGAA	600
Db	1387	TTGGAAGGTAAAGTGGATAAAAAATGTTTTGCAGATAGCCTTGAGCAAATAATCACGAA	1446
Qy	601	AAAGATAGTGAAAGCAGTAATGATGACACTTCATTTCCAGTACACCAGAAGCTGTAAGA	660
Db	1447	AAAGATAGTGAGAGTAGTAATGATGATACTTCTTTCCCAGTACGCCAGAAGGTATAAAG	1506
Qy	661	GGTGGTTCCGGAGCGTACATCACGTGTGCTCCCTTTAACC---CAACAACAGAGAATGTT	717
Db	1507	GATCGTTCAGGAGCATATATCACATGTGCTCCCTTTAACCAGCAGCAACTGAGAGCATT	1566
Qy	718	TCAACAAACATTTTTCCCTTGTTGGAAGATCATACTTCGAAAAATAAGACAGATGAAAAA	777
Db	1567	GSOURCE: 4251TTTCCCTTTGTTAGGAGATCCTACTTCAGAAAAATAAGACCGATGAAAAA	1626
Qy	778	AAGATAGAA-AAAAAAGGCCAAATTGTAACAGAGAAGAATGCAAGTGTCAAGACATCA	836
Db	1627	AAAATAGAAGAAAAGAAGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAAACATCA	1686
Qy	837	AACCCTTTCCTTATGGCAGCACAGGAGTCTAAGACAGATTACGTTACAACAGATCATGTG	896
Db	1687	AACCCTTTCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATTTA	1746
Qy	897	TCAAAGGTGACCGAGGAAGTAGTGGCAAACATGCCTGAAGGTCTAACCCAGATTTGGTT	956
Db	1747	ACAAAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTA	1806
Qy	957	CAGGAAGCATGTGAAAGTGAATTGAATGAAGCTACTGGTACAAAAATTGCCTTTGAAACA	1016
Db	1807	CAGGAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACA	1866
Qy	1017	AAAATGGACCTGGTTCAAACCTCAGAAGCTGTGCAGGAGTCACTTTACCCTGTAACACAG	1076
Db	1867	AAAATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAG	1926
Qy	1077	CTTTGCCCATCTTTTGAAGAATCTGAAGCTACTCCGTCACCGTTTTGCCTGACATTGTC	1136
Db	1927	CTTTGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGCCTGACATTGTT	1986
Qy	1137	ATGGAAGCACCATTAAATTTCTGTAGTTCCTAGTGCTGGTGCTTCTGCAGTGCAGCTCAGT	1196
Db	1987	ATGGAAGCACCATTGAATTTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCAGC	2046
Qy	1197	TCATCACCATTAGAAACTCTTCCTTCAGTTAATTATGAAAGCATAAAGTTTGAGCCTGAA	1256
		AAT	
Db	2047	TCATCACCATTAGAAGC---TTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAA	2103
Qy	1257	AATCCCCCACCATATGAGGAGGCCATGAATGTATCACTAAAAAAGAATCAGGAATGAAT	1316
Db	2104	AACCCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAG	2163
Qy	1317	GAAGAAATCACAGAGCCTGAAGGTATTAGTGTAGCTGTTGAGGAAACAGAAGCTCCTTAT	1376
Db	2164	GAAGAAATTAAAGAGCCTGAAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTAT	2223

Qy	1377	ATATCTATTGTCATGTGATTTAATTAAAGAAAACAAAGATCTCTACTGAACCGACTCCAGAT	1436
Db	2224		
Qy	1437	TTCTCTAGTTATTTCAGAAATAGCAGAAGTTGCACAGCCAGTGCCCGAGCATTCTGAGCTA	1496
Db	2284		
Qy	1497	GTGAAGATTCCTCCCCGATTCTGAACCAGTTGACTTATTTAGTGTATGATTCAATACCC	1556
Db	2344		
Qy	1557	GAAGTTCCACAAAAACAAGATGAAGCTGTAATACTTGTGAAAGAAAACCTCACTGAAATT	1616
Db	2404		
Qy	1617	TCATCTGAGTCAATGACAGGACATGACAATAAGGGAAAACTCAGTGCCTTACCATCACCT	1676
Db	2464		
Qy	1677	GAGGGAGGAAAACCGTATTTGGAGTCTTTTCAGCCCAGTTTAGGCATCACAAAAGATACC	1736
Db	2521		
Qy	1737	TTAGCACCTGATGAAGTTTCAGCATTGACCCAAAAGGAGAAAATCCCTTTGCAGATGGAG	1796
Db	2581		
Qy	1797	GAGCTCAATACTGCAGTTTATTCAAGTGATGGCTTATTCATTGCTCAGGAAGCAAACCTA	1856
Db	2641		
Qy	1857	AGAGAAAGTGAAACATTTTCAGATTTCATCTCCGATTGAGATTATAGATGAGTTCCCGACC	1916
Db	2701		
Qy	1917	TTTGTCAGTTCTAAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACACTGACCTAGAA	1976
Db	2761		
Qy	1977	GTAGCCCAACAAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTCATTGGCTTGTGCA	2036
Db	2821		
Qy	2037	GGATTGCCCCATGACCTTTCTTTCAAGAGTATACAACC-----TAAAGAGGAAGTTCAT	2090
Db	2881		
Qy	2091	GTCCCGATGAGTTCTCCAAAGATAGGGGTGATGTTTCAAAGGTGCCCGTACTGCCTCCA	2150
Db	2941		
Qy	2151	GATGTTTCTGCTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAAACCCAAAGTTCTT	2210
Db	3001		
Qy	2211	GTGAAAGAAGCCGAGAGAAAACTTCTTCTGATACAGAAAAAGAGCGAAGATCTCCATCT	2270

Db	3061	 GTGAAAGAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCT	3120
Qy	2271	 GCTATATTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGAC	2330
Db	3121	 GCTATATTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGAC	3180
Qy	2331	 ATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTGTTTCCTGCTGCTCTCGCTGACAGTA	2390
Db	3181	 ATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTCTGCTGCTTTTCATTGACAGTA	3240
Qy	2391	 TTCAGCATTGTGAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCTGTGACTATCAGC	2450
Db	3241	 TTCAGCATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGC	3300
Qy	245		
Db	3301	 TTTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTCT	3360
Qy	2511	 AGGGCATATTTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTTCTGAGTACAGCAAT	2570
Db	3361	 AGGGCATATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTTCTGAGTACAGTAAT	3420
Qy	2571	 TCTGCTCTTGGTCATGTAACTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGTTGAT	2630
Db	3421	 TCTGCTCTTGGTCATGTGAACCTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGAT	3480
Qy	2631	 GATTTAGTTGATTCTCTGAAGTTTGCACTGTTGATGTGGGTATTTACCTATGTTGGTGCC	2690
Db	3481	 GATTTAGTTGATTCTCTGAAGTTTGCACTGTTGATGTGGGTATTTACCTAT	540
Qy	2691	 TTGTTCAATGGTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCCTGTT	2750
Db	3541	 TTGTTTAAATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCTGTT	3600
Qy	2751	 ATTTATGAACGGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTT	2810
Db	3601	 ATTTATGAACGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTT	3660
Qy	2811	 AAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGA	2870
Db	3661	 AAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGA	3720
Qy	2871	 GAAAGCCTGAAAGAGTTAAACAATAGAGGAGTTTATCTTTAAAGGGGATATTCAATTTGATT	2930
Db	3721	 AAACGCCCAAAATAATTAGT-----AGGAGTTTCATCTTTAAAGGGGATATTCAATTTGATT	3775
Qy	2931	 CCATTGGGGAGGGTCAGGGAAGAACAAGCCTTGACATTGCAGTGCAGTTTCACAGATCT	2990
Db	3776	AT-----ATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGGCCAATTCATTC	3810
Qy	2991	 TTATTTTGTAGCAACGCAGTG-TCTGAGGAAAAATGACCTGTCTTGAAGTGCCTGTGTTCA	3049
Db	3786	 TTATTTTGTAGCCATGCACTGTTGTGAGGAAAAATTACCTGTCTTGAAGTGCCTGTGTTCA	3845
Qy	3050	 TCATCTTAAGTATTGTAAGCTGCTATGTATGGATTAAATCGTAATCATATTTGTTTTTC	3109


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; Sequence 5, Application US/09758140
; Patent No. US20020012965A1
; GENERAL INFORMATION:
; APPLICANT: Strittmatter, Stephen M.
; TITLE OF INVENTION: No. US20020012965A1o Receptor-Mediated Blockade of
Axonal Growth
; FILE REFERENCE: 44574-5073-US
; CURRENT APPLICATION NUMBER: US/09/758,140
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/175,707
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: US 60/207,366
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,378
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 4053
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (135)..(3710)
; OTHER INFORMATION: Human mRNA for No. US20020012965A1o protein (KIAA0886,
GenBank
; OTHER IN
US-09-758-140-5

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Query Match G DATE: cc62s10p 88co0820020042965A19AB020698h 4053;
Best Local Similarity 86.6%; Pred. No. 0;
Matches 2802; Conservative 0; Mismatches 381; Indels 54; Gaps 14;

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Qy      1 CTATCTCCTCTCTCAGCCGCTGCTTTTAAAGAACGTGAATACCTTGGTGATTACCAGCA 60
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Db      846 CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAATTTGTCAACA 905

Qy      61 GTACTGCCCACTGAAGGAACACTTCCAGCAACTTCAAATGAAGCTTCTAAAGCATTCTCA 120
      ||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      906 GTATTACCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA 965

Qy      121 GAGAAGGCAAAAAATCCATTGTAGAGAGAAATTTAACAGAATTTTCAGAATTGGAATAT 180
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      966 GAGAA      AAACTCTACTCATAGATAGAGATTTAACAGAGTTTTCAGAATTAGAATAC 1005

Qy      181 TCAGAAATGGAATCATCATTAGTGGCTCTCAAAGGCAGAACCTGCCGTAACAGTAGCG 240
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1026 TCAGAAATGGGATCATCGTTCAGTGTCTCTCAAAGGCAGAACTGCGCGTAATAGTAGCA 1085

Qy      241 AATCCTAGGGACGAAATAGTTGTGAGGAGTAGAGATAAAGAAGAGGACTTAGTTAGTCTT 300
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1086 AATCCTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGTTAGTTAGTAAT 1145

Qy      301 AACATCCTTCATACTCAGCAGGAGTTATCTACAGTCCTTACGAAATCAGTTGAAGAAGAA 360
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1146 AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT 1205

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Qy	361	GATAGAGTTCTGTCTCCAGCAAAAAACAAAGGACAGTTTTAAGGAAAAGGGAGTTGCAGCA	420
Db	1206	GA---AGTTGTGTCTTCAGAAAAAGCAAAAGACAGTTTTAATGAAAAGAGAGTTGCAGTG	1262
Qy	421	GAAGCTTCTATGGGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG	480
Db	1263	GAAGCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG	1322
Qy	481	AAAGATACTTACAAGCAAGATAGTGATGTTTTGATTGCTGGAGGTAATATAGAGAGCAAA	540
Db	1323	AAAGATAGT---AAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAATCGAGAGCAAC	1379
Qy	541	TTGGAAGGTAAAGTGGATAAGAAACACTTTTTCAGATAGCCTTGAACAAACAAATCGTGAA	600
Db	1380	AAGTGGATAAAAAATGTTTTTCAGATAGAGGTTGAGCAAACTAATCACGAA	1439
Qy	601	AAAGATAGTGAAAGCAGTAATGATGACACTTCATTTCCAGTACACCAGAAGCTGTAAGA	660
Db	1440	AAAGATAGTGAGAGTAGTAATGATGATACTTCTTCCCCAGTACGCCAGAAGGTATAAAG	1499
Qy	661	GGTGGTTCGGAGCGTACATCACGTGTGCTCCCTTTAACC---CAACAAGTGAAGTGT	717
Db	1500	GATCGTTTCAGGAGCATATATCACATGTGCTCCCTTTAACCAGCAGCAACTGAGAGCATT	1559
Qy	718	TCAACAAACATTTTTCCTTGTGGAAGATCATACTTCGGAATAAGACAGATGAAAAA	777
Db	1560	GCAACAAACATTTTTCCTTTGTTAGGAGATCCTACTTCAGAAAATAAGACCGATGAAAAA	1619
Qy	778	AAGATAGAA-AAAAAAGGCACAAATTGTAACAGAGAAGAATGCAAGTGTCAAGACATCA	836
Db	1620	AAAATAGAAGAAAAGAAGGCCAAATAGTAACAGAGAAGAATACTAGCACCAAAACATCA	1679
Qy	837	AACCCTTTCTTATGGCAGCACAGGAGTCTAAGACAGATTACGTTACAACAGATCATGTG	896
Db	1680	AACCCTTTTCTGTAGCAGCACAGGATTCTGAGACAGATTATGTCAACAGATAATTTA	1739
Qy	897	TCAAAGGTGACCGAGGAAGTAGTGGCAAACATGCCTGAAGGTCTAACCCAGATTTGGTT	956
Db	1740	ACAAAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTA	1799
Qy	957	CAGGAAGCATGTGAAAGTGAATTGAATGAAGCTACTGGTACAAAAATTGCCTTTGAAACA	1016
Db	1800	CAGGAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACA	1859
Qy	1017	AAAATGGACCTGGTTCAAACCTTCAGAAGCTGTGCAGGAGTCACTTTACCCTGTAACACAG	1076
Db	1860	AAAATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCTGCAGCACAG	1919
Qy	1077	CTTTGCCCATCTTTTGAAGAATCTGAAGCTACTCCGTCACCGTTTTGCCTGACATTGTC	1136
Db	1920	CTTTGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGCCTGACATTGTT	1979
Qy	1137	ATGGAAGCACCATTAATTTCTGTAGTTCCTAGTGCTGGTGCTTCTGCAGTGCAGCTCAGT	1196
Db	1980	ATGGAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCAGC	2039
Qy	1197	TCATCACCATTAGAACTCTTCTTCAGTTAATTATGAAAGCATAAAGTTTGAGCCTGAA	1255

Db	2040	TCATCACCATTAGAAGC---TTCTTCAGTTAATTATGAAAGCATAAAAACATGAGCCTGAA	2096
Qy	1257	AATCCCCCACCATATGAGGAGGCCATGAATGTATCACTAAAAAAGAATCAGGAATGAAT	1316
Db	2097	AACCCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAG	2156
Qy	1317	GAAGAAATCACAGAGCCTGAAGGTATTAGTGTAGCTGTTCAAGAAACAGAAGCTCCTTAT	1376
Db	2157	GAAGAAATTAAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTAT	2216
Qy	1377	ATATCTATTGCATGTGATTTAATTAAAGAAACAAAGATCTCTACTGAACCGACTCCAGAT	1436
Db	2217	ATATCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCAGCTCCGAT	2276
Qy	143		
Db	2277	TTCTCTGATTATTTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCCTGATCATTCTGAGCTA	2336
		ATTCAGAAATAGCAGAAGTTGCACAGCCAGTGCCCGAGCATTCAGAGAAA	599650XC
Qy	1497	GTTGAAGATTCCCTCCCCGATTCTGAACAGTTGACTTATTTAGTGATGATTCAATACCC	1556
Db	2337	GTTGAAGATTCCCTCACCTGATTCTGAACAGTTGACTTATTTAGTGATGATTCAATACCT	2396
Qy	1557	GAAGTTCCACAAAAACAAGATGAAGCTGTAATACTTGTGAAAGAAAACCTCACTGAAATT	1616
Db	2397	GACGTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACT	2456
Qy	1617	TCATCTGAGTCAATGACAGGACATGACAATAAGGGAAAACTCAGTGCTTCACCATCACCT	1676
Db	2457	TCATTTGAGTCAATGATAGAATATGAAAATAAGGAAAAACTCAGTGCTTTG8---CACCT	2513
Qy	1677	GAGGGAGGAAAAACCGTATTTGGAGTCTTTTCAGCCCAGTTTAGGCATCACAAAAGATACC	1736
Db	2514	GAGGGAGGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACC	2573
Qy	1737	TTAGCACCTGATGAAGTTTCAGCATTGACCCAAAAGGAGAAAAATCCCTTTGCAGATGGAG	1796
Db	2574	CTGTTACCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAAATTCCTTTGCAGATGGAG	2633
Qy	1797	GAGCTCAATACTGCAGTTTATTCAAGTGATGGCTTATTCATTGCTCAGGAAGCAAACCTA	1856
Db	2634	GAGCTCAGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATA	2693
Qy	1857	AGAGAAAAGTGAAACATTTTCAGATTTCATCTCCGATTGAGATTATAGATGAGTTCCCGACC	1916
Db	2694	AGAGAAAAGTGAAACGTTTTTCATTCTCTCCAATTGAAATTATAGATGAGTTCCCTACA	2753
Qy	1917	TTTGTCAGTTCTAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACACTGACCTAGAA	1976
Db	2754	TTGATCAGTTCTAAAACTGATTCAATTTCTAAATTAGCCAGGGAATATACTGACCTAGAA	2813
Qy	1977	GTAGCCCACAAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTCATTGGCTTGTGCA	2036
Db	2814	GTATCCCACAAAAGTGAAATTGCTAATGCCCGGATGGAGCTGGGTCATTGCCTTGCACA	2873
Qy	2037	GGATTGCCCCATGACCTTTCTTTCAAGAGTATACAACC-----TAAAGAGGAAGTTCAT	2090

Db	2874	GAATTGCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGT	2933	
Qy	2091	GTCCCAGATGAGTTCTCCAAAGATAGGGGTGATGTTTCAAAGGTGCCCGTACTGCCTCCA	2150	
Db	2934	TTCTCAGATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCA	2993	
Qy	2151	GATGTTTCTGCTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAAACCCAAAGTTCTT	2210	
Db	2994	GATGTTTCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTT	3053	
Qy	2211	GTGAAAGAAGCCGAGAGAAAACTTCCTTCTGATACAGAAAAAGAGCGAAGATCTCCATCT	2270	
Db	3054	GTGAAAGAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCT	3113	
Qy	2271	GCTATATTTTTCAGCAGAGCTGAGTAAAACCTTCAGTTGTTGACCTCCTCTACTGGAGAGAC	2330	
Db	3114	GCTATATTTTTCAGCAGAGCTGAGTAAAACCTTCAGTTGTTGACCTCCTGTACTGGAGAGAC	3173	
Qy	2331	ATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTGTTCTCTGCTGCTCTCGCTGACAGTA	2390	
Db	3174	ATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTATTCTCTGCTGCTTTTCATTGACAGTA	3233	
Qy	2391	TTCAGCATTGTGAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCTGTGACTATCAGC	2450	
Db	3234	TTCAGCATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGC	3293	
Qy	2451	TTTAGGATATATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATTC	2510	
Db	3294	TTTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTC	3353	
Qy	2511	AGGATCTCTTCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCA5XA	2570	
Db	3354	AGGGCATATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTTCAGAAGTACAGTAAT	3413	
Qy	2571	TCTGCTCTTGGTCATGTTAACTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGTTGAT	2630	
Db	3414	TCTGCTCTTGGTCATGTGAACTGCACGATAAAAGGAACTCAGGCGCCTCTTCTTAGTTGAT	3473	
Qy	2631	GATTTAGTTGATTCTCTGAAGTTTGCAGTGTGATGTGGGTATTTACCTATGTTGGTGCC	2690	
Db	3474	GATTTAGTTGATTCTCTGAAGTTTGCAGTGTGATGTGGGTATTTACCTATGTTGGTGCC	3533	
Qy	2691	TTGTTCAATGGTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCCTGTT	2750	
Db	3534	TTGTTTAATGGTCTGACACTACTGATTTTGGCTCTCATTTCACCTCTTCAGTGTTCCTGTT	3593	
Qy	2751	ATTTATGAACGGCATCA1	AAATAGATCATTATCTGGGACTTGCAAATAAGGATGTT	2810
Db	3594	ATTTATGAACGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTT	3653	
Qy	2811	AAAGATGCTATGGCTAAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGA	2870	
Db	3654	AAAGATGCTATGGCTAAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGAATGA	3713	
Qy	2871	GAAAGCCTGAAAGAGTTAAACAATAGAGGAGTTTATCTTTAAAGGGGATATTCAATTGATT	2930	
Db	3714	AAACGCCCAAAATAATTA-----GTAGGAGTTCATCTTTAAAGGGGATATTCAATTGATT	3766	


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Qy      2931 CCATTGGGGAGGGTCAGGGAAGAACAAAGCCTTGACATTGCAGTGCAGTTTCAC----- 2984
      |  |||||||||||||||||||  ||  |||||||  |||||||||||||||||||
Db      3769 ATACGGGGGAGGGTCAGGGAAGAACGAA-CCTTGACGTTGCAGTGCAGTTTCACAGATCG 3827

Qy      2985 -----AGATCTTTATTTTGTAGCAACGCAGTG-TCTGAGGAAAAATGACCTGTCTTGA CTG 3038
      |||||||||||||||||||  ||  ||  ||  |||||||||||||||||||
Db      3828 TTGTTAGATCTTTATTTTGTAGCCATGCACTGTTGTGAGGAAAAATTACCTGTCTTGA CTG 3887

Qy      3039 CCCTGTGTTTCATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTTAAATCGTAATCAT 3098
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Db      3888 CCATGTGTTTCATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTTAAACCGTAATCAT 3947

Qy      3099 ATTTGTTTTTTCCTGTATGAGGCACTGGTGAATAAAACAAAGATCTGAGAAAGCTGTATATT 3158
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Db      1      8 A--TCTTTTTTCTATCTGAGGCACTGGTGA-----AAATGAAAAAAGCTGTATATT 3994

Qy      3159 ACACTTTGTGCGCAGGTAGTCTTGCTGTAT-TTGGGGAATTGCAAAGAAAGTGGAGCT 3214
      |||||||  ||||  |||||||  ||  ||  ||||  |  |||||  ||  |||||||
Db      3995 TTACTTTGTTGCAGATAGTCTTGCCGCATCTTGGCAAGTTGCAGAGATGGTGGAGCT 4051

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RESULT 3

US-09-972-599A-5

; Sequence 5, Application US/09972599A

; Patent No. US20020077295A1

; GENERAL INFORMATION:

; APPLICANT: STRITTMATTER, STEPHEN M.

; TITLE OF INVENTION: NOGO-RECEPTOR-MEDIATED BLOCKADE OF AXONAL GROWTH

; FILE REFERENCE: C077 CIP US

; CURRENT APPLICATION NUMBER: US/09/972,599A

; CURRENT FILING DATE: 2001-10-06

; PRIOR APPLICATION NUMBER: PCT/US01/01041

; PRIOR FILING DATE: 2001-01-12

; PRIOR APPLICATION NUMBER: 09/758,140

; PRIOR FILING DATE: 2001-01-12

; PRIOR APPLICATION NUMBER: 60/236,378

; PRIOR FILING DATE: 2000-09-29

; PRIOR APPLICATION NUMBER: 60/207,366

CCT5 418

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: 60/175,707

; PRIOR FILING DATE: 2000-01-12

; NUMBER OF SEQ ID NOS: 57

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 5

; LENGTH: 4053

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (135)..(3710)

; OTHER INFORMATION: Human DNA encoding for No. US20020077295A1o protein (KIAA0886, GenBank

; OTHER INFORMATION: Accession No. US20020077295A1 AB020693)

US-09-972-599A-5

Query Match

62.1%; Score 2379.4; DB 9; Length 4053;

Best Local Similarity 86.6%; Pred. No. 0;
Matches 2802; Conservative 0; Mismatches 381; Indels 54; Gaps 14;

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Qy      1 CTATCTCCTCTCTCAGCCGCTGCTTTTAAAGAACGTGAATACCTTGGTGATTTACCAGCA 60
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Db     846 CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAATTTGTCAACA 905

Qy     61 GTACTGCCCCACTGAAGGAACACTTCCAGCAACTTCAAATGAAGCTTCTAAAGCATTCTCA 120
      ||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     906 GTATTACCCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA 965

Qy    121 GAGAAGGCAAAAAATCCATTTGTAGAGAGAAATTTAACAGAATTTTCAGAATTGGAATAT 180
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    966 GAGAAGGCAAAAACTCTACTCATAGATAGAGATTTAACAGAGTTTTTCAGAATTAGAATAC 1025

Qy    181 TCAGAAATGGAATCATCATTTCAGTGGCTCTCAAAA4          TGCCGTAACAGTATG 240
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Db   1026 TCAGAAATGGGATCATCGTTTCAGTGTCTCTCCAAAAGCAGAATCTGCCGTAATAGTAGCA 1085

Qy    241 AATCCTAGGGACGAAATAGTTGTGAGGAGTAGAGATAAAGAAGAGGACTTAGTTAGTCTT 300
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Db   1086 AATCCTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGTTAGTTAGTAAT 1145

Qy    301 AACATCCTTCATACTCAGCAGGAGTTATCTACAGTCCTTACGAAATCAGTTGAAGAAGAA 360
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Db   1146 AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT 1205

Qy    361 GATAGAGTTCTGTCTCCAGAAAAAACAAGGACAGTTTTAAAGGAAAAGGGAGTTGCAGCA 420
      ||  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   1206 GA---AGTTGTGTCTTCAGAAAAAGCAAAGACAGTTTTAAATGAAAAGAGAGTTGCAGTG 1262

Qy    421 GAAGCTTCTATGGGGGAGGAATATGCAGACTTCAAACCATTGAGCGAGTATGGGAAGTG 480
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   1263 GAAGCTCCTATGAGGGGAGGAATATGCAGACTTCAAACCATTGAGCGAGTATGGGAAGTG 1322

Qy    481 AAAGATACTTACAAGCAAGATAGTGATGTTTTGATTGCTGGAGGTAATATAGAGAGCAAA 540
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   1323 AAAGATAGT---AAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAAATCGAGAGCAAC 1379

Qy    541 TTGGAAGGTAAAGTGGATAAGAAACACTTTTCAGATAGCCTTGAACAAACAAATCGTGAA 600
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Db   1380 TTGGAAGGTAAAGTGGATAAAAAATGTTTTGCAGATAGCCTTGAACAACTAATCACGAA 1439

Qy    601 AAAGATAGTGAAAGCAGTAATGATGACACTTCATTTCCCAGTACACCAGAAGCTGTAAGA 660
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   1440 AAAGATAGTGAGAGTAGTAATGATGATACTTCTTTCCCAGTACGCCAGAAGGTATAAAG 1499

Qy    661 GGTGGTTCCGGAGCGTACATCACGTGTGCTCCCTTTAACC---CAACAACTGAGAATGTT 717
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Db   1500 GATCGTTTCAGGAGCATATATCACATGTGCTCCCTTTAACCAGCAGCAACTGAGAGCATT 1559

Qy    718 TCAACAAACATTTTTCCTTGTGGAAGATCATACTTCGGAAAAATAAGACAGATGAAAAA 777
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Db   1560 GCAACAAACATTTTTCCTTTGTTAGGAGATCCTACTTCAGAAAAATAAGACCGATGAAAAA 1619

Qy    778 AAGATAGAA-AAAAAAGGCACAAATTGTAACAGAGAAGAATGCAAGTGTCAAGACATCA 836
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Db 1620 AAAATAGAAGAAAAGAAGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAACATCA 1679

Qy 837 AACCCCTTTCCTTATGGCAGCACAGGAGTCTAAGACAGATTACGTTACAACAGATCATGTG 896
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Db 1680 AACCCCTTTCCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATTTA 1739

Qy 897 TCAAAGGTGACCGAGGAAGTAGTGGCAAACATGCCTGAAGGTCTAACCCCAGATTTGGTT 956
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Db 1740 ACAAAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTA 1799

Qy 957 CAGGAAGCATGTGAAAGTGAATTGAATGAAGCTACTGGTACAAAAATTGCCTTTGAAACA 1016
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Db 1800 CAGGAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACA 1859

Qy 1017 AAAATGGACCTGGTTCAAACCTCAGAAGCTGTGCAGGAGTCACTTTACCCGTGAACACAG 1076
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Db 1860 AAAATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAG 1919

Qy 1077 CTTTGCCCATCTTTTGAAGAATCTGAAGCTACTCCGTCACCGGTTTTGCCTGACATTGTC 1136
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Db 1920 CTTTGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGCCTGACATTGTT 1979

Qy 1137 ATGGAAGCACCATTAAATTCTGTAGTTCCTAGTGCTGGTGCTTCTGCAGTGCAGCTCAGT 1196
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Db 1980 ATGGAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCAGC 2039

Qy 1197 TCATCACCATTAGAACTCTTCCTTCAGTTAATTATGAAAGCATAAAGTTTGAGCCTGAA 1256
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Db 2040 TCATCACCATTAGAAGC---TTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAA 2096

Qy 1257 AATCCCCCACCATATGAGGAGGCCATGAATGTATCACTAAAAAAGAATCAGGAATGAAT 1316
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Db 2097 AACCCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAG 2156

Qy 1317 GAAGAAATCACAGAGCCTGAAGGTATTAGTGTAGCTGTTTCAGGAAAAGAGCTCCTTAT 1376
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Db 2157 GAAGAAATTAAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAAAGAGCTCCTTAT 2216

Qy 1377 ATATCTATTGCATGTGATTTAATTAAAGAAACAAAGATCTCTACTGAACCGACTCCAGAT 1436
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Db 2217 ATATCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCAGCTCCGGAT 2276

Qy 1437 TTCTCTAGTTATTTCAGAAATAGCAGAAGTTGCACAGCCAGTGCCCGAGCATTCCTGAGCTA 1496
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Db 2277 TTCTCTGATTATTTCAGAAATGGCAAAGTTGAACAGCCAGTGCTGATCATTCCTGAGCTA 2336

Qy 1497 GTTGAAGATTTCCTCCCCGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCC 1556
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Db 2337 GTTGAAGATTTCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCT 2396

Qy 1557 GAAGTTCCACAAAAACAAGATGAAAGCTGTAATACTTGTGAAAGAAAACCTCACTGAAATT 1616
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Db 2397 GACGTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACT 2456

Qy 1617 TCATCTGAGTCAATGACAGGACATGACAATAAGGGAAAACTCAGTGCTTCACCATCACCT 1676
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Db 2457 TCATTTGAGTCAATGATAGAATATGAAAATAAGGAAAACTCAGTGCTTTGC---CACCT 2513

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 Db 2514 GAGGGAGGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACC 2573

Qy 1737 TTAGCACCTGATGAAGTTTCAGCATTGACCCAAAAGGAGAAAATCCCTTTGCAGATGGAG 1796
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 Db 2574 CTGTTACCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAATTCCTTTGCAGATGGAG 2633

Qy 1797 GAGCTCAATACTGCAGTTTATTCAAGTGATGGCTTATTTCATTGCTCAGGAAGCAAACCTA 1856
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 Db 2634 GAGCTCAGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATA 2693

Qy 1857 AGAGAAAGTGAAACATTTTCAGATTTCATCTCCGATTGAGATTATAGATGAGTTCCCGACC 1916
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 Db 2694 AGAGAAACTGAAACGTTTTCAGATTTCATCTCCAATTGAAATTATAGATGAGTTCCCTACA 2753

Qy 1917 TTTGTCAGTTCTAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACACTGACCTAGAA 1976
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 Db 2754 TTGATCAGTTCTAAACTGATTTCATTTCTAAATTAGCCAGGGAATATACTGACCTAGAA 2813

Qy 1977 GTAGCCCACAAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTCATTGGCTTGTGCA 2036
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 Db 2814 GTATCCCACAAAAGTGAAATTGCTAATGCCCGGATGGAGCTGGGTCATTGCCTTGCACA 2873

Qy 2037 GGATTGCCCCATGACCTTTCTTTCAAGAGTATACAACC-----TAAAGAGGAAGTTCAT 2090
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 Db 2874 GAATTGCCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGT 2933

Qy 2091 GTCCCAGATGAGTTCTCCAAAGATAGGGGTGATGTTTCAAAGGTGCCCGTACTGCCTCCA 2150
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 Db 2934 TTCTCAGATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCA 2993

Qy 2151 GATGTTTCTGCTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAAACCCAAAGTTCTT 2210
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 Db 2994 GATGTTTCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTT 3053

Qy 2211 GTGAAAGAAGCCGAGAGAAAACTTCCTTCTGATACAGAAAAAGAGCGAAGATCTCCATCT 2270
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 Db 3054 GTGAAAGAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCT 3113

Qy 2271 GCTATATTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGAC 2330
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 Db 3114 GCTATATTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGAC 3173

Qy 2331 ATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTGTTCTGCTGCTCTCGCTGACAGTA 2390
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 Db 3174 ATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTCTGCTGCTTTTCATTGACAGTA 3233

Qy 2391 TTCAGCATTGTGAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCTGTGACTATCAGC 2450
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 Db 3234 TTCAGCATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGC 3293

Qy 2451 TTTAGGATATATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATTC 2510
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 Db 3294 TTTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTC 3353

Qy	2511	AGGGCATATTTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGCAAT	2570
Db	3354	AGGGCATATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAAT	3413
Qy	2571	TCTGCTCTTGGTCATGTTAACTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGTTGAT	2630
Db	3414	TCTGCTCTTGGTCATGTGAACTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGAT	3473
Qy	2631	GATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCC	2690
Db	3474	GATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCC	3533
Qy	2691	TTGTTCAATGGTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCCCTGTT	2750
Db	3534	TT GTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCCTGCTT	3593
Qy	2751	ATTTATGAACGGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTT	2810
Db	3594	ATTTATGAACGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTT	3653
Qy	2811	AAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGA	2870
Db	3654	AAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGAATGA	3713
Qy	2871	GAAAGCCTGAAAGAGTTAACAATAGAGGAGTTTATCTTTAAAGGGGATATTCATTTGATT	2930
Db	3714	AAACGCCCAAATAATTA-----GTAGGAGTTTCATCTTTAAAGGGGATATTCATTTGATT	3768
Qy	2931	CCATTGGGGAGGGTCAGGGAAGAACAAAGCCTTGACATTGCAGTGCAGTTTCAC-----	2984
Db	3769	ATACGGGGGAGGGTCAGGGAAGAACGAA-CCTTGACGTTGCAGTGCAGTTTCACAGATCG	3827
Qy	2985	-----AGATCTTTATTTTATAGCAACGCAGTG-TCTGAGGAAAAATGACCTGTCTTGACTG	3038
Db	3828	TTGTTAGATCTTTATTTTATAGCCATGCAGTGTTGTGAGGAAAAATTACCTGTCTTGACTG	3887
Qy	3039	CCCTGTGTTTCATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTTAAATCGTAATCAT	3098
Db	3888	CCATGTGTTTCATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTTAAACCGTAATCAT	3947
Qy	3099	ATTTGTTTTTCTGTATGAGGCACTGGTGAATAAAACAAAGATCTGAGAAAGCTGTATATT	3158
Db	3948	A--TC'TTTTTCTATCTGAGGCACTGGTGA-----ATAAAAAACCTGTATATT	3994
Qy	3159	ACACTTTGTGCGCAGGTAGTCTTGCTGTAT-TTGGGGAATTGCAAAGAAAGTGGAGCT	3214
Db	3995	TTACTTTGTTGCAGATAGTCTTGCCGCATCTTGGCAAGTTGCAGAGATGGTGGAGCT	4051

CTTAAG 3 4 25X1

RESULT 4

US-09-789-386-1

; Sequence 1, Application US/09789386

; Patent No. US20020010324A1

; GENERAL INFORMATION:

; APPLICANT: MICHALOVICH, DAVID

; APPLICANT: PRINJHA, RABINDER KUMAR

; TITLE OF INVENTION: NOVEL COMPOUNDS

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; FILE REFERENCE: GP-30165-C1
; CURRENT APPLICATION NUMBER: US/09/789,386
; CURRENT FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: U.K. 9916898.1
; PRIOR FILING DATE: 1999-07-19
; PRIOR APPLICATION NUMBER: U.K. 9816024.5
; PRIOR FILING DATE: 1998-07-22
; PRIOR APPLICATION NUMBER: US 09/359,208
; PRIOR FILING DATE: 1999-07-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 3579
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-789-386-1
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Query Match          58.0%; Score 2223.6; DB 9; Length 3579;
Best Local Similarity 87.5%; Pred. No. 0;
Matches 2519; Conservative 0; Mismatches 339; Indels 22; Gaps 7;
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Qy      1 CTATCTCCTCTCTCAGCCGCTGCTTTTAAAGAACGTGAATACCTTGGTGATTACCAGCA 60
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Db      712 CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAATTTGTCAACA 771

Qy      61 GTACTGCCCACTGAAGGAACACTTCCAGCAACTTCAAATGAAGCTTCTAAAGCATCTCTCA 120
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Db      772 GTATTACCCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA 831

Qy      121 GAGAAGGCCAAAAATCCATTTGTAGAGAGAAATTTAACAGAAATTTTCAGAAATTGGAATAT 180
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      832 GAGAAGGCCAAAACTCTACTCATAGATAGAGATTTAACAGAGTTTTCAGAAATTAGAATAC 891

Qy      181 TCAGAAATGGAATCATCATTCAGTGGCTCTCAAAGGCAGAACCTGCCGTAACAGTAGCG 240
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Db      892 TCAGAAATGGGATCATCGTTCAGTGTCTCTCCAAAGCAGAAATCTGCCGTAATAGTAGCA 951

Qy      241 AATCCTAGGGACGAAATAGTTGTGAGGAGTAGAGATAAAGAAGAGGACTTAGTTAGTCTT 300
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Db      952 AATCCTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGTTAGTTAGTAAT 1011

Qy      301 AACATCCTTCATACTCAGCAGGAGTTATCTACAGTCCTTACGAAATCAGTTGAAGAAGAA 360
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Db      1012 AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT 1071

Qy      361 GATAGAGTTCTGTCTCCAGAAAAAACAAAGGACAGTTTTTAAGGAAAAGGGAGTTGCAGCA 420
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Db      1072 GA---AGTTGTGTCTTCAGAAAAAGCAAAAGACAGTTTTTAATGAAAAGAGAGTTGCAGTG 1128

Qy      421 GAAGCTTCTATGGGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG 480
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Db      1129 GAAGCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG 1188

Qy      481 AAAGATACTTACAAGCAAGATAGTGATGTTTTGATTGCTGGAGGTAATATAGAGAGCAAA 540
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Db      1189 AAAGATAGT---AAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAATCGAGAGCAAC 1245
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Db	2143	TTCTCTGATTATTTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCTA	2202
Qy	1497	GTTGAAGATTCCCTCCCCGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCC	1556
Db	2203	GTTGAAGATTCCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCT	2262
Qy	1557	GAAGTTCCACAAAAACAAGATGAAGCTGTAATACTTGTGAAAGAAAACCTCAGTGAATTT	1616
Db	2263	GACGTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCTCAGTGAAGCT	2322
Qy	1617	TCATCTGAGTCAATGACAGGACATGACAATAAGGGAAAACCTCAGTGCCTTACCATCACCT	1676
Db	2323	TCATTTGAGTCAATGATAGAATATGAAAATAAGGAAAAACCTCAGTGCCTTGC---CACCT	2379
Qy	1677	GAGGGAGGAAAAACCGTATTTGGAGTCTTTTCAGCCCAGTTTAGGCATCACAAAAGATACC	1736
Db	2380	GAGGGAGGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACC	2439
Qy	1737	TTAGCACCTGATGAAGTTTCAGCATTGACCCAAAAGGAGAAAATCCCTTTGCAGATGGAG	1796
Db	2440	CTGTTACCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAATTCCTTTGCAGATGGAG	2499
Qy	1797	GAGCTCAATACTGCAGTTTATTCAAGTGATGGCTTATTCAATTGCTCAGGAAGCAAACCTA	1856
Db	2500	GAGCTCAGTACTGCAGTTTATTCAAGTGATGGCTTATTCAATTGCTCAGGAAGCAAACCTA	2559
Qy	1857	AGAGAAAGTGAAACATTTTCAGATTTCATCTCCGATTGAGATTATAGATGAGTTCCCGACC	1916
Db	2560	AGAGAAACTGAAACGTTTTCAGATTTCATCTCCAATTGAAATTATAGATGAGTTCCCTACA	2619
Qy	1917	TTTGTTCAGTTCTAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACACTGACCTAGAA	1976
Db	2620	TTGATCAGTTCTAAAACTGATTTCATTTTCTAAATTAGCCAGGGAATATACTGACCTAGAA	2679
Qy	1977	GTAGCCCAAAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTCATTGGCTTGTGCA	2036
Db	2680	GTATCCCAAAAAGTGAAATTGCTAATGCCCCGATGGAGCTGGGTCATTGCCCTGCACA	2739
Qy	2037	GGATTGCCCCATGACCTTTCTTTCAAGAGTATACAACC-----TAAAGAGGAAGTTCAT	2090
Db	2740	GAATTGCCCCATGACCTTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGT	2799
Qy	2091	GTCCCAGATGAGTTCTCCAAAGATAGGGGTGATGTTTCAAAGGTGCCCGTACTGCCTCCA	2150
Db	2800	TTCTCAGATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCA	2859
Qy	2151	GATGTTTCTGCTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAAACCCAAAGTTCTT	2210
Db	2860	GATGTTTCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTT	2919
Qy	2211	GTGAAAGAAGCCGAGAGAAAACTTCTTCTGATACAGAAAAAGAGCGAAGATCTCCATCT	2270

Db	2920	GTGAAAGAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCT	2979
Qy	2271	GCTATATTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGAC	2330
Db	2980	GCTATATTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGAC	3039
Qy	2331	ATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTGTTCTGCTGCTCTCGCTGACAGTA	2390
Db	3040	ATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTATTCCTGCTGCTTTTCATTGACAGTA	3099
Qy	2391	TTCAGCATTGTGAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCTGTGACTATCAGC	2450
Db	3100	TTCAGCATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGC	3159
Qy	2451	TTTAGGATATATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATTC	2510
Db	3160	TTTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTC	3219
Qy	2511	AGGGCATATTTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGCAAT	2570
Db	3220	AGGGCATATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAAT	3279
Qy	2571	TCTGCTCTTGGTCATGTTAACTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGTTGAT	2630
Db	3280	TCTGCTCTTGGTCATGTGAAGTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGAT	3339
Qy	2631	GATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCC	2690
Db	3340	GATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCC	3399
Qy	2691	TTGTTCAATGGTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCCCTGTT	2750
Db	3400	TTGTTTAATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCCTGTT	3459
Qy	2751	ATTTATGAACGGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTT	2810
Db	3460	ATTTATGAACGGCATCAGGCGCAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTT	3519
Qy	2811	AAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGA	2870
Db	3520	AAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGAATGA	3579

RESULT 5

US-09-893-348-22

; Sequence 22, Application US/09893348

; Patent No. US20020072493A1

; GENERAL INFORMATION:

; APPLICANT: EISENBACH-SCHWARTZ, Michal

; APPLICANT: COHEN, Irun R.

; APPLICANT: BESERMAN, Pierre

; APPLICANT: MOSONEGO, Alon

; APPLICANT: MOALEM, Gila

; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USES

; FILE REFERENCE: EIS-SCHWARTZ=2A

; CURRENT APPLICATION NUMBER: US/09/893,348

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; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/314,161
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 09/218,277
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: PCT/US98/14715
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: IL 124500
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 3579
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3579)
; OTHER INFORMATION:
US-09-893-348-22

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Query Match          58.0%; Score 2223.6; DB 9; Length 3579;
Best Local Similarity 87.5%; Pred. No. 0;
Matches 2519; Conservative 0; Mismatches 339; Indels 22; Gaps 7;

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Qy      1 CTATCTCCTCTCTCAGCCGCTGCTTTTAAAGAACGTGAATACCTTGGTGATTTACCAGCA 60
      || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      712 CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAATTTGTCAACA 771

Qy      61 GTACTGCCCACTGAAGGAACACTTCCAGCAACTTCAAATGAAGCTTCTAAAGCATTCTCA 120
      ||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      772 GTATTACCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA 831

Qy      121 GAGAAGGCAAAAAATCCATTTGTAGAGAGAAATTTAACAGAATTTTCAGAATTGGAATAT 180
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      832 GAGAAGGCAAAAACTCTACTCATAGATAGAGATTTAACAGAGTTTTCAGAATTAGAAATAC 891

Qy      181 TCAGAAATGGAATCATCATTCAGTGGCTCTCAAAGGCAGAACCTGCCGTAACAGTAGCG 240
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      892 TCAGAAATGGGATCATCGTTCAGTGTCTCTCCAAAAGCAGAATCTGCCGTAATAGTAGCA 951

e Qy      omo 841 AATCCTAGGGAAGAAATAATCGTGAAAATAAAGATGAAGAAGAGAGTGTCTT 300
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      952 AATCCTAGGGAAGAAATAATCGTGAAAATAAAGATGAAGAAGAGAGTGTCTT 1011

Qy      301 AACATCCTTCATACTCAGCAGGAGTTATCTACAGTCCTTACGAAATCAGTTGAAGAAGAA 360
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1012 AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT 1071

Qy      361 GATAGAGTTCTGTCTCCAGAAAAACAAAGGACAGTTTTAAGGAAAAGGGAGTTGCAGCA 420
      || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1072 GA---AGTTGTGTCTTCAGAAAAAGCAAAGACAGTTTTAATGAAAAGAGAGTTGCAGTG 1128

Qy      421 GAAGCTTCTATGGGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG 480
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1129 GAAGCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG 1188

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Qy	481	AAAGATACTTACAAGCAAGATAGTGTATGTTTTGATTGCTGGAGGTAATATAGAGAGCAAA	540
Db	1189	AAAGATAGT--AAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAATAATCGAGAGCAAC	1245
Qy	541	TTGGAAGGTAAAGTGGATAAGAAACACTTTTCAGATAGCCTTGAACAAACAAATCGTGAA	600
Db	1246	TTGGAAGGTAAAGTGGATAAAAAATGTTTTGCAGATAGCCTTGAGCAAATAATCACGAA	1305
Qy	601	AAAGATAGTGAAAGCAGTAATGATGACACTTCATTTCCCAGTACACCAGAAGCTGTAAGA	660
Db	1306	AAAGATAGTGAGAGTAGTAATGATGATACTTCTTTCCCAGTACGCCAGAAGGTATAAAG	1365
Qy	661	GGTGGTTCCGGAGCGTACATCACGTGTGCTCCCTTTAACC---CAACAAGTGAAGATGTT	717
Db	1366	GATCGTCCAGGAGCATATATCATGTGCTCCCTTTAACCAGCAGCAACTGAGAGCATT	1425
Qy	718	TCAACAAACATTTTTCCCTTGTTGGAAGATCATACTTCGGAAAAATAAGACAGATGAAAAA	777
Db	1426	GCAACAAACATTTTTCTTTGTTAGGAGATCCTACTTCAGAAAAATAAGACCGATGAAAAA	1485
Qy	778	AAGATAGAA-AAAAAAGGCACAAATTGTAACAGAGAAGAATGCAAGTGTCAAGACATCA	836
Db	1486	AAAATAGAAGAAAAGAAGGCCAAATAGTAACAGAGAAGAACTAGCACCAAAACATCA	1545
Qy	837	AACCCCTTCTCTTATGGCAGCACAGGAGTCTAAGACAGATTACGTTACAACAGATCATGTG	896
Db	1546	AACCCCTTCTCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCAACAGATAATTTA	1605
Qy	897	TCAAAGGTGACCGAGGAAGTAGTGCCAAACATGCCTGAAGGTCTAACCCAGATTTGGTT	956
Db	1606	ACAAAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCTGACTCCAGATTTAGTA	1665
Qy	957	CAGGAAGCATGTGAAAGTGAATTGAATGAAGCTACTGGTACAAAAATTGCCTTTGAAACA	1016
Db	1666	CAGGAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACA	1725
Qy	1017	AAAATGGACCTGGTTCAAACCTCAGAAGCTGTGCAGGAGTCACTTTACCTGTAAACAG	1076
Db	1726	AAAATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAG	1785
Qy	1077	CTTTGCCCATCTTTTGAAGAATCTGAAGCTACTCCGTCACCGGTTTTGCCTGACATTGTC	1136
Db	1786	CTTTGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTACCAGTTTTGCCTGACATTGTT	1845
Qy	1137	ATGGAAGCACCATTAAATTCTGTAGTTCCTAGTGCTGGTGCTTCTGCAGTGCAGCTCAGT	1196
Db	1846	ATGGAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCAGC	1905
Qy	1197	TCATCACCATTAGAAACTCTTCCCTCAGTTAATTATGAAAGCATAAAGTTTGAGCCTGAA	1256
Db	1906	TCATCACCATTAGAAGC---TTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAA	1962
Qy	1257	AATCCCCCACCATATGAGGAGGCCATGAATGTATCACTAAAAAAGAATCAGGAATGAAT	1316
Db	1963	AACCCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAG	2022
Qy	1317	GAAGAAATCACAGAGCCTGAAGGTATTAGTGTAGCTGTTCAGGAAACAGAAGCTCCTTAT	1376

Db	2023	GAAGAAATTAAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTAT	2082
Qy	1377	ATATCTATTGCATGTGATTTAATTAAAGAAACAAAGATCTCTACTGAACCGACTCCAGAT	1436
Db	2083	ATATCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCAGCTCCGGAT	2142
Qy	1437	TTCTCTAGTTATTCAGAAATAGCAGAAGTTGCACAGCCAGTGCCCGAGCATTCTGAGCTA	1496
Db	2143	TTCTCTGATTATTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCTA	2202
Qy	1497	GTTGAAGATTCTCCCCGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCC	1556
Db	2203	GTTGAAGATTCTCTACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCT	2262
Qy	1557	GAAGTTCCACAAAAACAAGATGAAGCTGTAATACTTGTGAAAGAAAACCTCACTGAAATT	1616
Db	2263	GACGTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACT	2322
Qy	1617	TCATCTGAGTCAATGACAGGACATGACAATAAGGGAAAACTCAGTGCTTCACCATCACCT	1676
Db	2323	TCATTTGAGTCAATGATAGAATATGAAAATAAGGAAAACTCAGTGCTTTGC---CACCT	2379
Qy	1677	GAGGGAGGAAAACCGTATTTGGAGTCTTTTCAGCCCAGTTTAGGCATCACAAAAGATACC	1736
Db	2380	GAGGGAGGAAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACC	2439
Qy	1737	TTAGCACCTGATGAAGTTTCAGCATTGACCCAAAAGGAGAAAAATCCCTTTGCAGATGGAG	1796
Db	2440	CTGTTACCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAAATCCCTTTGCAGATGGAG	2499
Qy	1797	GAGCTCAATACTGCAGTTTATTCAAGTGATGGCTTATTCATTGCTCAGGAAGCAAACCTA	1856
Db	2500	GAGCTCAGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATA	2559
Qy	1857	AGAGAAAGTGAAACATTTTCAGATTATCTCCGATTGAGATTATAGATGAGTTCCCGACC	1916
Db	2560	AGAGAAACTGAAACGTTTTTCAGATTATCTCCAATTGAAATTATAGATGAGTTCCCTACA	2619
Qy	1917	TTTGTCAGTTCTAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACACTGACCTAGAA	1976
Db	2620	TTGATCAGTTCTAAAACTGATTCAATTTCTAAATTAGCCAGGGAATATACTGACCTAGAA	2679
Qy	1977	GTAGCCCAAAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTTCATTGGCTTGTGCA	2036
Db	2680	GTATCCCAAAAAGTGAAATTGCTAATGCCCGGATGGAGCTGGGTTCATTGCCTTGACA	2739
Qy	2037	GGATTGCCCCATGACCTTTCTTTCAAGAGTATACAACC-----TAAAGAGGAAGTTCAT	2090
Db	2740	GAATTGCCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGT	2799
Qy	2091	GTCCCAGATGAGTTCTCCAAAGATAGGGGTGATGTTTCAAAGGTGCCCCGACTGCCTCCA	2150
Db	2800	TTCTCAGATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCA	2859
Qy	2151	GATGTTTCTGCTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAAACCCAAAGTTCTT	2210


```

; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND
THEIR USES
; FILE REFERENCE: EIS-SCHWARTZ=2A
; CURRENT APPLICATION NUMBER: US/09/893,348
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/314,161
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 09/218,277
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: PCT/US98/14715
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: IL 124500
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 4684
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (253)..(3744)
; OTHER INFORMATION:
US-09-893-348-17

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Qy	1	CTATCTCCTCTCTCAGCCGCTGCTTTTAAAGAACATGGAATACCTTGGTGATTTACAGCA	60
Db	928	CTATCTCCTCTCTCAACTGTTTCTTTTAAAGAACATGGATACCTTGGTAACTTATCAGCA	987
Qy	61	GTA CTGCCCCACTGAAGGAACACTTCCAGCAACTTCAAATGAAGCTTCTAAAGCATTCTCA	120
Db	988	GTGTCATCCTCAGAAGGAACAATTGAAGAACTTTAAATGAAGCTTCTAAAGAGTTGCCA	1047
Qy	121	GAGAAGGCCAAAAAATCCATTTGTAGAGAGAAAATTTAACAGAATTTTCAGAATTGGAATAT	180
Db	1048	GAGAGGGCAACAAATCCATTGTAAATAGAGATTTAGCAGAATTTTCAGAATTAGAATAT	1107
Qy	181	TCAGAAATGGAATCATCATTCACTGGCTCTCAAAGGCAGAACCTGCCGTAACAGTAGCG	240
Db	1108	TCAGAAATGGGATCATCTTTTAAAGGCTCCCCAAAGGAGAGTCAGCCATATTAGTAGAA	1167
Qy	241	AATCCTAGGGACGAAATAGTTGTGAGGAGTAGAGATAAAGAAGAGGACTTAGTTAGTCTT	300
Db	1168	AACACTAAGGAAGAAGTAATTGTGAGGAGTAAAGACA--AAGAGGATTTAGTTTGTAGT	1224
Qy	301	AACATCCTTCATACTCAGCAGGAGTTATCTACAGTCCTTACGAAATCAGTTGAAGAAGAA	360
Db	1225	GCAGCCCTTCACAGTCCACAAGAATCACCT-----GTGGGTAAAGAA	1266
Qy	361	GATAGAGTTCTGTCTCCAGAAAAAACAAAGGACAGTTTTTAAGGAAAAGGGAGTTGCAGCA	420
Db	1267	GACAGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTTAATGAAATGCAGATGTCAGTA	1326

[illegible]

Db	2152	 CCCCCACCATATGAAGAAGCCATGAATGTAGCACT--AAAAGCTTTGGGAACAAAGGAA	2208
Qy	1320	GAAATCACAGAGCCTGAAGGTATTAGTGTAGCTGTTTCAGGAAACAGAAGCTCCTTATATA	1379
Db	2209	 GGAATAAAAGAGCCTGAAAGTTTAAATGCAGCTGTTTCAGGAAACAGAAGCTCCTTATATA	2268
Qy	1380	TCTATTGCATGTGATTTAATTAAAGAAACAAAGATCTCTACTGAACCGACTCCAGATTTTC	1439
Db	2269	 TCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTTC	2328
Qy	1440	TCTAGTTATTTCAGAAATAGCAGAAGTTGCACAGCCAGTGCCCGAGCATTCTGAGCTAGTT	1499
Db	2329	 TCTAATTATTTCAGAAATAGCAAAATTTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTG	2388
Qy	1500	GAAGATTCTCTCCCGATTCTGAACCAAGTTGACTTATTTAGTGATGATTCAATACCCGAA	1559
Db	2389	 GAGGATTCTCTCACCTGAATCTGAACCAAGTTGACTTATTTAGTGATGATTTCGATTCTTGAA	2448
Qy	1560	GTTCCACAAAAACAAGATGAAGCTGTAATACTTGTGAAAGAAAACCTCACTGAAATTTCA	1619
Db	2449	 GTCCACAAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGAAGTGTC-	2507
Qy	1620	TCTGAGTCAATGACAGGACATGACAATAAGGGAAACTCAGTGCTTCACCATCACCTGAG	1679
Db	2508	-----TGAGACAGTAGCCAGCACAAAGAGGAGAGACTTAGTGCCTCAC---CTCAGGAG	2559
Qy	1680	GGAGGAAAACCGTATTTTGAGTCTTTTCAGCCAGTTTAGGCATCACAAAAGATACCTTA	1739
Db	2560	 CTAGGAAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAAAAGATGC---T	2616
Qy	1740	GCACCTGATGAAGTTTTCAGCATTGACCCAAAAGGAGAAAAATCCCTTTGCAGATGGAGGAG	1799
Db	2617	 GCATCTAATGACATTCCAACATTGACCAAAAAGGAGAAAAATTTCTTTGCAATGGAAGAG	2676
Qy	1800	CTCAATACTGCAGTTTATTCAAGTGATGGCTTATTCAITGCTCAGGAAGCAAACTAAGA	1859
Db	2677	 TTTAATACTGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGACAAAATAAAA	2736
Qy	1860	GAAAGTGAAACATTTTTCAGATTCTCTCCGATTGAGATTATAGATGAGTTCCCGACCTTT	1919
Db	2737	 GAAAGTGAAACATTTTTCAGATTCTCTCCGATTGAGATAATAGATGAATTTCCACGTTT	2796
Qy	1920	GTCAGTTCTAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACACTGACCTAGAAGTA	1979
Db	2797	 GTCAGTGCTAA--AGATGATTCTCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTA	2853
Qy	1980	GCCCACAAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTCAATTGGCTTGTGCAGGA	2039
Db	2854	 TCCGACAAAAGTGAAATTGCTAATATCCAAAGCGGGCAGATTCAATTGCCTTGCTTAGAA	2913
Qy	2040	TTGCCCCATGACCTTTCTTTCAAGAGTATACAACCTAAAGAGGAAGTTCATGTCCAGAT	2099
Db	2914	 TTGCCCTGTGACCTTTCTTTCAAGAATATATATCCTAAAGATGAAGTACATGTTTCAGAT	2973
Qy	2100	GAGTTCTCCAAAGATAGGGGTGATGTTTCAAAGGTGCCCGTACTGCCTCCAGATGTTTCT	2159

Db	2974	GAATTCTCCGAAAAATAGGTCCAGTGTATCTAAGGCATCCATATCGCCTTCAAATGTCTCT	3033
Qy	2160	GCTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAAACCCAAAGTTCTTGTGAAAGAA	2219
Db	3034	GCTTTGGAACCTCAGACAGAAATGGGCAGCATAGTTAAATCCAAATCACTTACGAAAGAA	3093
Qy	2220	GCCGAGAGAAAACTTCTCTTGATACAGAAAAAGAGCGAAGATCTCCATCTGCTATATTT	2279
Db	3094	GCAGAGAAAAAACTTCTCTTGACACAGAGAAAGAGGACAGATCCCTGTCAGTGTATTG	3153
Qy	2280	TCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAG	2339
Db	3154	TCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAG	3213
Qy	2340	ACTGGAGTGGTGTGTTTGGTGCCAGCTTGTTCTGCTGCTCTCGCTGACAGTATTCAGCATT	2399
Db	3214	ACTGGAGTGGTGTGTTTGGTGCCAGCTTATTCCTGCTGCTGTCTCTGACAGTGTTCAGCATT	3273
Qy	2400	GTGAGTGTAACGGCCTACATTGCCTTGCCCTGCTCTCTGTGACTATCAGCTTTAGGATA	2459
Db	3274	GTCAGTGTAACGGCCTACATTGCCTTGCCCTGCTCTCGGTGACTATCAGCTTTAGGATA	3333
Qy	2460	TATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATTCAAGGGCATAT	2519
Db	3334	TATAAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCCACCCATTCAAGGGCATAT	3393
Qy	2520	TTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGCAATTCTGCTCTT	2579
Db	3394	TTAGAATCTGAAGTTGCTATATCAGAGGAATTGGTTCAGAAATACAGTAAATCTGCTCTT	3453
Qy	2580	GGTCATGTAACTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGTTGATGATTTAGTT	2639
Db	3454	GGTCATGTGAACAGCACACAATAAAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTTAGTT	3513
Qy	2640	GATTCTCTGAAGTTTGTCAGTGTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTCAAT	2699
Db	3514	GATTCCCTGAAGTTTGTCAGTGTGATGTGGGTGTTTACTTATGTTGGTGCCTTGTTCAAT	3573
Qy	2700	GGTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCCTGTTATTTATGAA	2759
Db	3574	GGTCTGACACTACTGATTTTAGCTCTGATCTCACTCTTCAGTATTCCTGTTATTTATGAA	3633
Qy	2760	CGGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAAATGTTAAAGATGCT	2819
Db	3634	CGGCATCAGGTGCAGATAGATCATTATCTAGGACTTGCAAACAAGAGTGTTAAGGATGCC	3693
Qy	2820	ATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGAGAAAGCCTG	2879
Db	3694	ATGGCCAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCAGATTGAAAAAGCCCC	3753
Qy	2880	AAAGAGTTAACAATAGAGGAGTTTATCTTTAAAGGGGATATTCATTTGATTCCATTGGGG	2939
Db	3754	AA-----ACAGAAGTTCATCTTTAAAGGGGACACTCACTTGATTAC---GGG	3797
Qy	2940	AGGGTCAGGGAAGAACAAGCCTTGACATTGCAGTGCAGTTTCACAGATCTTTATTTTTTA	2999
Db	3798	GGTGGGAGGGTCAGGGGTGAGCCCTTGGTGGCCGTGCGGTTT--CAGCTCTTTATTTTTA	3855

[illegible]

Qy 3825 AAAAAAAAAA 3833
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 Db 4674 AAAAAAAAAA 4682

RESULT 7

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US-10-220-891-22
; Sequence 22, Application US/10220891
; Publication No. US20030207286A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWARA, AKIRA
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES HAVING CHARACTERITICS OF ENHANCED
; TITLE OF INVENTION: EXPRESSION IN HUMAN NEUROBLASTOMA WITH FAVORABLE
PROGNOSIS
; TITLE OF INVENTION: BASED ON COMPARISON BETWEEN HUMAN NEUROBLASTOMA WITH
FAVORABLE
; TITLE OF INVENTION: PROGNOSIS AND HUMAN NEUROBLASTOMA WITH UNFAVORABLE
PROGNOSIS
; FILE REFERENCE: 7388-73435
; CURRENT APPLICATION NUMBER: US/10/220,891
; CURRENT FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: JP 2000/140387
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: JP 2000/159195
; PRIOR FILING DATE: 2000-03-07
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
; LENGTH: 1980
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-220-891-22

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Query Match 36.9%; Score 1414.6; DB 13; Length 1980;
Best Local Similarity 87.0%; Pred. No. 0;
Matches 1671; Conservative 0; Mismatches 209; Indels 41; Gaps 9;

Qy	1326	ACAGAGCCTGAAGGTATTAGTGTAGCTGTTCAAGAAACAGAAGCTCCTTATATATCTATT	1385
Db	28	AAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTATATATCTATT	87
Qy	1386	GCATGTGATTTAATTAAAGAAACAAAGATCTCTACTGAACCGACTCCAGATTTCTCTAGT	1445
Db	88	GCATGTGATTTAATTAAAGAAACAAAGCTTTCCTGCTGAACCAGCTCCGATTTCTCTGAT	147
Qy	1446	TATTCAGAAATAGCAGAAGTTGCACAGCCAGTGCCCCGAGCATTCTGAGCTAGTTGAAGAT	1505
Db	148	TATTCAGAAATGGCAAAGTTGAACAGCCAGTG CCTGATCATTTCTGAGCTAGTTGAAGAT	207
Qy	1506	TCCTCCCCCGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCCGAAGTTCCA	1565
Db	208	TCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCTGACGTTCCA	267
Qy	1566	CAAAAACAAGATGAAGCTGTAATACTTGTGAAAGAAAACCTCACTGAAATTT CATCTGAG	1625
Db	268	CAAAAACAAGGTGAAA CTGTGATGCTTGTGAAAGAAAAGTCTCACTGAGACTTCATTTGAG	327

[illegible]

Db	1165	 TACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTAGGGGCATAT	1224
Qy	2520	TTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGCAATTCTGCTCTT	2579
Db	1225	 CTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTT	1284
Qy	2580	GGTCATGTTAACCTGCACAATAAAAAGAACTCAGACGCCTCTTCTTAGTTGATGATTTAGTT	2639
Db	1285	 GGTCATGTGAACCTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTT	1344
Qy	2640	GATTCTCTGAAGTTTGCAGTGTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTCAAT	2699
Db	1345	 GATTCTCTGGAGTTTGCAGTGTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAAAT	1404
Qy	2700	GGTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCCTGTTATTTATGAA	2759
Db	1405	 GGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCTGTTATTTATGAA	1464
Qy	2760	CGGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTTAAAGATGCT	2819
Db	1465	 CGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTTAAAGATGCT	1524
Qy	2820	ATGGCTAAAATCCAAGCAAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGAGAAAGCCTG	2879
Db	1525	 ATGGCTAAAATCCAAGCAAAAAATCCCTGGATTGAAGCGCAAAGCTGAATGAAAACGCCCA	1584
Qy	2880	AAAGAGTTAACAATAGAGGAGTTTATCTTTAAAGGGGATATTCAATTTGATTCCATTGGGG	2939
Db	1585	 AAATAATTA-----GTAGGAGTTCATCTTTAAAGGGGATATTCAATTTGATTATACGGGGG	1639
Qy	2940	AGGGTCAGGGAAGAACAAGCCTTGACATTGCAGTGCAGTTTCAC-----AGAT	2988
Db	1640	 AGGGTCAGGGAAGAACGAA-CTTGACGTTGCAGTGCAGTTTCACAGATCGTTGTTAGAT	1698
Qy	2989	CTTTATTTTGTAGCAACGCAGTG-TCTGAGGAAAAATGACCTGTCTTGACTGCCCTGTGTT	3047
Db	1699	 CTTTATTTTGTAGCCATGCACTGTTGTGAGGAAAAATTACCTGTCTTGACTGCCATGTGTT	1758
Qy	3048	CATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTTAAATCGTAATCATATTTGTTT-	3106
Db	1759	 CATCATCTTAAGTATTGTAAGCTGCTATGTATGGGTTTAAACCGTAATCATATCTTTTTC	1818
Qy	3107	-TTCCTGTATGAGGCACTGGTGAATAAAACAAGATCTGAGAAAGCTGTATATTACACTTT	3165
Db	1819	 CTATCTATCTGAGGCACTGGTGA-----ATAAAAAACCTGTATATTTTACTTT	1867
Qy	3166	GTCGCAGGTAGTCTTGCTGTAT-TTGGGGAATTGCAAAGAAAGTGGAGCTGACAGAAATA	3224
Db	1868	 GTTGCAGATAGTCTTGCCGCATCTTGGCAAGTTGCAGAGATGGTGGAGCTAGAAAAAAA	1927
Qy	3225	A 3225	
Db	1928	A 1928	

Db	1117	CTCATTTTCACTCTTTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT	1176
Qy	2784	TATCTGGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATC	2843
Db	1177	TATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATC	1236
Qy	2844	CCTGGATTGAAGCGTAAAGCTGAATGAGAAAAGCCTGAAAAGAGTTAACAATAGAGGAGTTT	2903
Db	1237	CCTGGATTGAAGCGCAAAGCTGAATGAAAACGCCCAAAATAATTA-----GTAGGAGTTC	1291
Qy	2904	ATCTTTTAAAGGGGATATTCAATTTGATTCCATTGGGGAGGGTCAGGGAAGAACAAGCCTT	2963
Db	1292	ATCTTTTAAAGGGGATATTCAATTTGATTATACGGGGGAGGGTCAGGGAAGAACGAA-CCTT	1350
Qy	2964	GACATTGCAGTGCAGTTTCAC-----AGATCTTTATTTTTAGCAACGCAGTG-T	3011
Db	1351	GACGTTGCAGTGCAGTTTCACAGATCGTTGTTAGATCTTTATTTTTAGCCATGCAGTGT	1410
Qy	3012	CTGAGGAAAAATGACCTGTCTTGACTGCCCTGTGTTCATCATCTTAAGTATTGTAAGCTG	3071
Db	1411	GTGAGGAAAAATTACCTGTC'TTGACTGCCATGTGTTCATCATCTTAAGTAT'TGTAAGCTG	1470
Qy	3072	CTATGTATGGATTTAAATCGTAATCATATTTGTTTTCCTGTATGAGGCACTGGTGAATA	3131
Db	1471	CTATGTATGGATTTAAACCGTAATCATA--TCTTTTTCCTATCTGAGGCACTGGTGAAT	1528
Qy	3132	AACAAAGATCTGAGAAAGC'TGTATATTACACTTTGTTCGCAGGTAGTCTTGCTGTAT-TTG	3190
Db	1529	AAAAAAC-----CTGTATATTTTACTTTGTTGCAGATAGTCTTGCCGCATCTTG	1577
Qy	3191	GGGAATTGCAAAGAAAGTGGAGCT-----GACAGAAATAACCCCTTTTCACAGTTTGTGC	3244
Db	1578	GCAAGTTGCAGAGATGGTGGAGCTAGAAAAAAAAAAAAAAAAAAGCCCTTTTCAGTTTGTGC	1637
Qy	3245	ACTGTGTACGGTCTGTGTAGGTTGATGCAGATTTTCTGAAATGAAA---TGTTTAGACG	3300
Db	1638	ACTGTGTATGGTCCGTGTAGATTGATGCAGATTTTCTGAAATGAAATGTTTGTTTAGACG	1697
Qy	3301	AGATCATGCCACCAAGGCAGGAGTGAAAAAGCTTGCCCTTTCCTGGTATGTTCTAGGTGTA	3360
Db	1698	AGATCATACCGGTAAAGCAGGAATGACAAAGCTTG-CTTTTCTGGTATGTTCTAGGTGTA	1756
Qy	3361	TTGTGAAATTTACTGTTGTATTAATTGCCAATATAAGTAAATATAGATTATATATATCTA	3420
Db	1757	TTGTGACTTTTACTGTTATATTAATTGCCAATATAAGTAAATATAGATTATA-----TA	1810
Qy	3421	TATATAGTGTTCACGAAGCTTAGCCCTTTACCTTCCCAGCTGCCCCACAGTGCTTGATA	3480
Db	1811	TGTATAGTGTTCACAAAGCTTAGACCTTTACCTT-CCAGCCACCCACAGTGCTTGATA	1869
Qy	3481	CT-----TCTGTTCATGGGTTTTATGTGTGTAGTCCCAAAGCACATAAGCTAGGGAGAAA	3534
Db	1870	TTTCAGAGTCAGTCATTGGTTATACATGTGTAGTTCCAAAGCACATAAGCTAGAAGAAGA	1929
Qy	3535	CGTACTTCTAGGCGCACTACCATCTGTTTTCAACACGAACCGACGCCATGCAAACAGAAC	3594
Db	1930	AATATTTCTAGGAGCACTACCATCTGTTTTCAACATGAA--ATGCCACACACATAGAAC	1986

Db	367	TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC	426
Qy	2484	CAGAAATCTGATGAAGGCCACCCATTTCAGGGCATATTTTGAATCTGAAGTTGCTATATCT	2543
Db	427	CAGAAATCAGATGAAGGCCACCCATTTCAGGGCATATCTGGAATCTGAAGTTGCTATATCT	486
Qy	2544	GAGGAGTTGGTTTCAAGTACAGCAATTCCTGCTCTTGGTCATGTTAACTGCACAATAAAA	2603
Db	487	GAGGAGTTGGTTTCAAGTACAGTAATTCCTGCTCTTGGTCATGTGAACTGCACGATAAAG	546
Qy	2604	GAACTCAGACGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTG	2663
Db	547	GAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTG	606
Qy	2664	ATGTGGGTATTTACCTATGTTGGTGCCTTGTTCATGGTCTGACACTACTAATTTTGGCT	2723
Db	607	ATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTCTGACACTACTGATTTTGGCT	666
Qy	2724	CTGATTTCACTCTTCAGTGTTTCTGTTATTTATGAACGGCATCAGGCGCAAATAGATCAT	2783
Db	667	CTCATTTCACTCTTCAGTGTTTCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT	726
Qy	2784	TATCTGGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATC	2843
Db	727	TATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATC	786
Qy	2844	CCTGGATTGAAGCGTAAAGCTGAATGAGAAAGCCTGAAAGAGTTAAACAATAGAGGAGTTT	2903
Db	787	CCTGGATTGAAGCGCAAAGCTGAATGAAAAAGCCCAAAAATAATTA-----GTAGGAGTTC	841
Qy	2904	ATCTTTTAAAGGGGATATTCATTTGATTCCATTTGGGGAGGGTCAGGGAAGAACAAGCCTT	2963
Db	842	ATCTTTTAAAGGGGATATTCATTTGATTATACGGGGAGGGTCAGGGAAGAACGAA-CCTT	900
Qy	2964	GACATTGCAGTGCAGTTTCAC-----AGATCTTTATTTTTAGCAACGCAGTGTCT	3012
Db	901	GACGTTGCAGTGCAGTTTCACAGATCGTTGTTAGATCTTTATTTTTAGCCATGCACTGTT	960
Qy	3013	-TGAGGAAAAATGACCTGTCTTGACTGCCCTGTGTTTCATCATCTTAAGTATTGTAAGCTG	3071
Db	961	GTGAGGAAAAATTACCTGTCTTGACTGCCATGTGTTTCATCATCTTAAGTATTGTAAGCTG	1020
Qy	3072	CTATGTATGGATTTAAATCGTAATCATATTTGTTTTTCTGTATGAGGCACTGGTGAATA	3131
Db	1021	CTATGTATGGATTTAAACCGTAATCATA--TCTTTTTCTATCTGAGGCACTGGTGA--	1076
Qy	3132	AACAAAGATCTGAGAAAGCTGTATATTACACTTTGTTCGAGGTAGTCTTGCTGTAT-TTG	3190
Db	1077	-----ATAAAAAACCTGTATATTTTACTTTGTTGCAGATAGTCTTGCCGCATCTTG	1127
Qy	3191	GGGAATTGCAAAGAAAGTGGAGCT-----GACAGAAATAACCCTTTTCAGTTTGTG	3243
Db	1128	GCAAGTTGCAGAGATGGTGGAGCTAGAAAAAAAAAAAAAAAAAGCCCTTTTCAGTTTGTG	1187
Qy	3244	CACTGTGTACGGTCTGTGTAGGTTGATGCAGATTTTCTGAAATGAAA----TGTTTAGAC	3299
Db	1188	CACTGTGTATGGTCCGTGTAGATTGATGCAGATTTTCTGAAATGAAATGTTTGTGTTAGAC	1247

; OTHER INFORMATION: Foocen-m2 reticulon
US-10-205-194-165

Query Match 21.6%; Score 826.4; DB 13; Length 2782;
Best Local Similarity 77.6%; Pred. No. 4.9e-196;
Matches 1231; Conservative 0; Mismatches 301; Indels 54; Gaps 17;

Qy	2263	CTCCATCTGCTATATTTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACT	2322
Db	1233	CTCTTCCTGCTGCATCTGAACCTGTGATACCTCCTCTGCAGTTGTTGACCTCCTCTACT	1292
Qy	2323	GGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTGTTCCCTGCTGCTCTCGC	2382
Db	1293	GGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTATTCCTGCTGCTGTCTC	1352
Qy	2383	TGACAGTATTCAGCATTGTGAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCTGTGA	2442
Db	1353	TGACAGTGTTCAGCATTGTGAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCGGTGA	1412
Qy	2443	CTATCAGCTTTAGGATATATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGGCC	2502
Db	1413	CTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCC	1472
Qy	2503	ACCCATTTCAGGGCATATTTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAAT	2562
Db	1473	ACCCATTTCAGGGCATATTTAGAATCTGAAGTTGCTATATCAGAGGAATTGGTTCAGAAAT	1532
Qy	2563	ACAGCAATTCTGCTCTTGGTTCATGTTAACTGCACAATAAAAGAACTCAGACGCCTCTTCT	2622
Db	1533	ACAGTAAATTCTGCTCTTGGTTCATGTGAACAGCACAATAAAAGAACTGAGGCGGCTTTTCT	1592
Qy	2623	TAGTTGATGATTTAGTTGATTCTCTGAAGTTTGAGTGTGATGTGGGTATTTACCTATG	2682
Db	1593	TAGTTGATGATTTAGTTGATTCCCTGAAGTTTGAGTGTGATGTGGGTGTTTACTTATG	1652
Qy	2683	TTGGTGCCTTGTTCAATGGTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTG	2742
Db	1653	TTGGTGCCTTGTTCAATGGTCTGACACTACTGATTTTAGCTCTGATCTCACTCTTCAGTA	1712
Qy	2743	TTCCTGTTATTTATGAACGGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAATA	2802
Db	1713	TTCCTGTTATTTATGAACGGCATCAGGTGCAGATAGATCATTATCTAGGACTTGCAAACA	1772
Qy	2803	AGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAG	2862
Db	1773	AGAGTGTAAAGGATGCCATGGCCAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAG	1832
Qy	2863	CTGAATGAGAAAGCCTGAAAGAGTTAAACAATAGAGGAGTTTATCTTTAAAGGGGATATTC	2922
Db	1833	CAGATTGAAAAAGCC-----CCAAAAGAGTTTCATCTTTAAAGGGGACACTC	1880
Qy	2923	ATTTGATTCCATTGGGGAGGGTCAGGGAAGAACAAAGCCTTGACATTGCAGTGCAGTTTC	2982
Db	1881	ACTTGATTAC----GGGGGTGGGAGGGTCAGGGGTGAGCCCTTGGTGGCCGTGCGGTTT-	1935
Qy	2983	ACAGATCTTTATTTTATGCAACGCAGTGTCTGAGGAAAAATGACCTGTCTTGACTGCCCT	3042

Db	1936	-CAGCTCTTTATTTTGTAGCAGTGCACCTGTTTGAGGAAAAATTACCTGTCTTGACT-TCCT	1993
Qy	3043	GTGTTTCATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTAAATCGTAATCATATTT	3102
Db	1994	GTGTTTATCATCTTAAGTATTGTAAGCTGCTGTGTATGGATCT-CATTGTAGTCACACTT	2052
Qy	3103	GTTTTTCCTGTATGAGGCACTGGTGAATAAAACAAAGATCTGAGAAAGCTGTATATTACAC	3162
Db	2053	GTCTTCCCAATGAGGCGCCTGGTGAATAAAGGAC--TCGGGGAAAGCTGTGCATTGTAT	2110
Qy	3163	TTTGTGCGCAGGTAGTCTTGCTGTATTTGGGGAATTGCAAAGAAAGTGGAGCT---GACAG	3219
Db	2111	CTGCTGCGCAGGGTAGTCTAGCTGTATGCAGAGAGTTGTAAAGAAGGCAAATCTGGGGGCAG	2170
Qy	3220	AAATAACCCCTTTTCACAGTTTGTGCACCTGTGTACGGTCTGTGTAGGTTGATGCAGATTTT	3279
Db	2171	GGAAAACCCCTTTTCACAG--TGTACTGTGTTTGGTCAGTGTAAACTGATGCAGATTTTTT	2228
Qy	3280	CTGAAATGAAATGTTTAGACGAGATCATGCCACCAAGGCAGGAGTGAAAAGCTTGCCTT	3339
Db	2229	CTGAAATGAAATGTTTAGATGAGAGCATACTACTAAAGCAGAGTGGAAGAACTCTGTC--T	2286
Qy	3340	TCCTGGTATGTTCTAGGTGTATTGTGAAATTTACTGTTGTATTAATTGCCAATATAAGTA	3399

Db	2287	TTATGGTGTGTTCTAGGTGTATTGTG-AATTTACTGTTAT---ATTGCCAATATAAGTA	2341
Qy	3400	AATATAGATTATATATATCTATATATAGTGTTTCACGAAGCTTAGCCCTTTACCTTCCCA	3459
Db	2342	AATATAGA----CCTAATCTATATATAGTGTTTCACAAAGCTTAGATCTTTAACCTTGCA	2397
Qy	3460	GCTGCCCCACAGTGCTTGATACTTCTGTTCATGGGTTTTATGTGTGTAGTCCCAAAGCACA	3519
Db	2398	GCTGCCCCACAGTGCTTGACCTCTGAGTCATTGGTTATGCAGTGTAGTCCCAAGCACATA	2457
Qy	3520	TAAGCTAGGGAGAAACGTACTTCTAGGCGCACTACC-ATCTGTTTTCAACACGAACCGAC	3578
Db	2458	AACTAGGAAGAGAAATGTATTTGTAGGAGTGCTACCTACCACCTGTTTTCAAGAAAATAT	2517
Qy	3579	GCCATGCAAACAGAACTCCTCAACATAAACTTCACTGCACAGACTTACTGTAGTTAATTT	3638
Db	2518	AGAACTCCAACAAAAATATAGAATGTCATTTCAAAGACTTACTGTATGTATAGTTAATTT	2577
Qy	3639	TATCACAAACTC-----TGGACTGAATCTAATGCTTCCAAAAATGTTTGCAAATA	3688
Db	2578	TGTCACAGACTCTGAAATTCTATGGACTGAATTTTCATGCTTCC--AAATGTTTGAGTTA	2635
Qy	3689	TCAAACATTGTTATGTAAGAAAATAT-AAATGACGATTTATACAATTGTGGTTTAAGCTG	3747
Db	2636	TCAAACATTGTTATGCAAGAAATCATAAAATGAAGACTTATACCATTGTGGTTTAAGCCG	2695
Qy	3748	TATTGAACTAAATCTGTGGAATGCATTGTGAACTGTAAAAGCAAAGTATCAATAAAGCTT	3807
Db	2696	TACTGAATT--ATCTGTGGAATGCATTGTGAACTGTAAAAGCAAAGTATCAATAAAGCTT	2753
Qy	3808	ATAGACTTAAAAAAAAAAAAAAAAAAAAA	3833
Db	2754	ATAGACTTAAAAAAAAAAAAAAAAAAAAA	2779

US-09-765-205-5

Query Match 17.9%; Score 685.8; DB 9; Length 1610;
Best Local Similarity 88.9%; Pred. No. 6.2e-161;
Matches 831; Conservative 0; Mismatches 72; Indels 32; Gaps 7;

Qy	2304	GTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGT'TTGGTGCCAGC	2363
Db	687	GTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGT'TTGGTGCCAGC	746
Qy	2364	TTGTTCCCTGCTGCTCTCGCTGACAGTATTTCAGCATTGTGAGTGTAAACGGCCTACATTGCC	2423
Db	747	CTATTCCTGCTGCTTTTCATTGACAGTATTTCAGCATTGTGAGCGTAACAGCCTACATTGCC	806
Qy	2424	TTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAGGCTATC	2483
Db	807	TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC	866
Qy	2484	CAGAAATCTGATGAAGGCCACCCATTTCAGGGCATATTTGGAATCTGAAGTTGCTATATCT	2543
Db	867	CAGAAATCAGATGAAGGCCACCCATTTCAGGGCATATCTGGAATCTGAAGTTGCTATATCT	926
Qy	2544	GAGGAGTTGGTTTCAGAAGTACAGCAATTCTGCTCTTGGTTCATGTTAACTGCACAATAAAA	2603
Db	927	GAGGAGTTGGTTTCAGAAGTACAGTAATTCTGCTCTTGGTTCATGTCAACTGCACGATAAAG	986
Qy	2604	GAAGTCAGACGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTG	2663
Db	987	GAAGTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTG	1046
Qy	2664	ATGTGGGTATTTACCTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTAATTTTGGCT	2723
Db	1047	ATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAAATGGTCTGACACTACTGATTTTGGCT	1106
Qy	2724	CTGATTTCACTCTTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCGCAAATAGATCAT	2783
Db	1107	CTCATTTCACTCTTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT	1166


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; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: US 60/349,936
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/361,834
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 156
; LENGTH: 1160
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-175-523-156
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Query Match          17.8%; Score 683; DB 15; Length 1160;
Best Local Similarity 88.6%; Pred. No. 2.5e-160;
Matches 830; Conservative 0; Mismatches 75; Indels 32; Gaps 7;
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Qy      2304 GTTGTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGC 2363
          |||
Db      228 GTTGTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGC 287

Qy      2364 TTGTTCCCTGCTGCTCTCGCTGACAGTATTTCAGCATTGTGAGTGTAAACGGCCTACATTGCC 2423
          ||
Db      288 CTATTCCTGCTGCTTTTCATTGACAGTATTTCAGCATTGTGAGCGTAACAGCCTACATTGCC 347

Qy      2424 TTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAGGCTATC 2483
          |||
Db      348 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC 407

Qy      2484 CAGAAATCTGATGAAGGCCACCCATTTCAGGGCATATTTGGAATCTGAAGTTGCTATATCT 2543
          |||
Db      408 CAGAAATCAGATGAAGGCCACCCATTTCAGGGCATATCTGGAATCTGAAGTTGCTATATCT 467

Qy      2544 GAGGAGTTGGTTCAGAAGTACAGCAATTCTGCTCTTGGTCATGTTAAGTGCACAATAAAA 2603
          |||
Db      468 GAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAAGTGCACGATAAAG 527

Qy      2604 GAACTCAGACGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAAGTGTG 2663
          |||
Db      528 GAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAAGTGTG 587

Qy      2664 ATGTGGGTATTTACCTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTAATTTTGGCT 2723
          |||
Db      588 ATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTCTGACACTACTGATTTTGGCT 647

Qy      2724 CTGATTTCACTCTTCAGTGTTTCTGTTATTTATGAACGGCATCAGGCGCAAATAGATCAT 2783
          ||
Db      648 CTCATTTCACTCTTCAGTGTTTCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT 707

Qy      2784 TATCTGGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATC 2843
          |||
Db      708 TATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATC 767

Qy      2844 CCTGGATTGAAGCGTAAAGCTGAATGAGAAAGCCTGAAAGAGTTAACAATAGAGGAGTTT 2903
          |||
Db      768 CCTGGATTGAAGCGCAAAGCTGAATGAAAACGCCCAAAATAATTA-----GTAGGAGTTC 822
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[illegible]

RESULT 13

US-09-789-386-3

; Sequence 3, Application US/09789386

; Patent No. US20020010324A1

; GENERAL INFORMATION:

; APPLICANT: MICHALOVICH, DAVID

; APPLICANT: PRINJHA, RABINDER KUMAR

10; TITLE OF INVENTION: NOVEL COMPOUNDS

; FILE REFERENCE: GP-30165-C1

; CURRENT APPLICATION NUMBER: US/09/789,386

; CURRENT FILING DATE: 2001-02-21

; PRIOR APPLICATION NUMBER: U.K. 9916898.1

; PRIOR FILING DATE: 1999-07-19

; PRIOR APPLICATION NUMBER: U.K. 9816024.5

; PRIOR FILING DATE: 1998-07-22

; PRIOR APPLICATION NUMBER: US 09/359,208

; PRIOR FILING DATE: 1999-07-22

; NUMBER OF SEQ ID NOS: 6

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; SOFTWARE: FastSEQ for Windows Version 3.0
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; SEQ ID NO 3

; LENGTH: 868

; TYPE: DNA

; ORGANISM: HOMO SAPIENS

; FEATURE:

; NAME/KEY: UNSURE

LOCATION: (91) (413)

US-09-789-386-3

Query Match 14.1%; Score 538.8; DB 9; Length 868;
Best Local Similarity 83.6%; Pred. No. 3e-124;
Matches 648; Conservative 0; Mismatches 118; Indels 9; Gaps 3;


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; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7385
; LENGTH: 4710
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-891-7385
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[illegible]

RESULT 15

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; Sequence 5, Application US/09789386
; Patent No. US20020010324A1
; GENERAL INFORMATION:
;   APPLICANT: MICHALOVICH, DAVID
;   APPLICANT: PRINJHA, RABINDER KUMAR
;   TITLE OF INVENTION: NOVEL COMPOUNDS
;   FILE REFERENCE: GP-30165-C1
;   CURRENT APPLICATION NUMBER: US/09/789,386
;   CURRENT FILING DATE: 2001-02-21
;   PRIOR APPLICATION NUMBER: U.K. 9916898.1
;   PRIOR FILING DATE: 1999-07-19
;   PRIOR APPLICATION NUMBER: U.K. 9816024.5
;   PRIOR FILING DATE: 1998-07-22
;   PRIOR APPLICATION NUMBER: US 09/359,208
;   PRIOR FILING DATE: 1999-07-22
;   NUMBER OF SEQ ID NOS: 6
;   SOFTWARE: FastSEQ for Windows Version 3.0
;   SEQ ID NO 5
;     LENGTH: 1122
;     TYPE: DNA
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; ORGANISM: HOMO SAPIENS
US-09-789-386-5

Query Match 13.7%; Score 527; DB 9; Length 1122;
Best Local Similarity 95.6%; Pred. No. 3.2e-121;
Matches 542; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

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Qy      2304 GTTGTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGC 2363
          |||
Db      556 GTTGTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGC 615

Qy      2364 TTGTTCCGCTGCTCTCGCTGACAGTATTGAGTGTGAGTGTACGGCCTACATTGCC 2423
          |||
Db      616 CTATTCCTGCTGCTTTCATTGACAGTATTGAGTGTGAGCGTAACAGCCTACATTGCC 675

Qy      2424 TTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAGGCTATC 2483
          |||
Db      676 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC 735

Qy      2484 CAGAAATCTGATGAAGGCCACCCATTGAGGCGATATTTGGAATCTGAAGTTGCTATATCT 2543
          |||
Db      736 CAGAAATCAGATGAAGGCCACCCATTGAGGCGATATCTGGAATCTGAAGTTGCTATATCT 795

Qy      2544 GAGGAGTTGGTTCAGAAGTACAGCAATTCTGCTCTTGGTCATGTAACTGCACAATAAAA 2603
          |||
Db      796 GAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAAGTGCACGATAAAG 855

Qy      2604 GAACTCAGACGCCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGAGTGTG 2663
          |||
Db      856 GAACTCAGGCGCCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGAGTGTG 915

Qy      2664 ATGTGGGTATTTACCTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTAATTTGGCT 2723
          |||
Db      916 ATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAAATGGTCTGACACTACTGATTTTGGCT 975

Qy      2724 CTGATTTCACTCTTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCGCAAATAGATCAT 2783
          |||
Db      976 CTCATTTCACTCTTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT 1035

Qy      2784 TATCTGGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATC 2843
          |||
Db      1036 TATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATC 1095

Qy      2844 CCTGGATTGAAGCGTAAAGCTGAATGA 2870
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Db      1096 CCTGGATTGAAGCGCAAAGCTGAATGA 1122
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Search completed: January 23, 2004, 15:24:49
Job time : 1162.34 secs

; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,580
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,568
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,314
; EARLIER FILING DATE: 1997-04-11
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; EARLIER FILING DATE: 1997-04-11
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; EARLIER APPLICATION NUMBER: 60/043,674
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,669
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,312
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; EARLIER APPLICATION NUMBER: 60/043,313
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; EARLIER APPLICATION NUMBER: 60/043,672
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,315
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/056,886
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,877
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,889
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,893
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,630
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,878
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,662
; EARLIER FILING DATE: 1997-08-22
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; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,882
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,637
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,903
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,888
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,879
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; EARLIER APPLICATION NUMBER: 60/056,880
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,894
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; EARLIER APPLICATION NUMBER: 60/056,911
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,636
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,874
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,910
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,864
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,631
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,845
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,892
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,761
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/047,595
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,599
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,588
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,585
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,586
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,590
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,594
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,589
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,593
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,614
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,578
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,576
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/047,501
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,670
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/056,632
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,664
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,876
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,881
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,909
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,875

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; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,862
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,887
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02
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Query Match          32.2%;  Score 227;  DB 4;  Length 168;
Best Local Similarity 60.0%;  Pred. No. 2.2e-19;
Matches    42;  Conservative    14;  Mismatches    14;  Indels      0;  Gaps      0;
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Qy      71 LLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIAKSDEGHPFRAYLESEVAISEE 130
      :|||| |::|| :|: ||||| ||||| ||||: ||:|||||:||||: :: :| |
Db      1 MLLSLAAFVSVISVSYLILALLSVTISFRIYKSVIQAVQKSEEGHPFKAYLDVDITLSSE 60

Qy      131 LVQKYSNSAL 140
      | |::|
Db      61 AFHNYMNAAM 70
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RESULT 8

US-08-905-223-411

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; Sequence 411, Application US/08905223
; Patent No. 6222029
; GENERAL INFORMATION:
;   APPLICANT: Edwards, Jean-Baptiste D.
;   APPLICANT: Duelert, Aymeric
;   APPLICANT: Lacroix, Bruno
;   TITLE OF INVENTION: 5' ESTs FOR SECRETED PROTEINS
;   NUMBER OF SEQUENCES: 503
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Knobbe, Martens, Olson & Bear
;     STREET: 501 West Broadway
;     CITY: San Diego
;     STATE: California
;     COUNTRY: USA
;     ZIP: 92101-3505
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy Disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: Win95
;     SOFTWARE: Word
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/905,223
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; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelsen, Ned A.
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 411:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 80 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
; ORIGINAL SOURCE:
; ORGANISM: Homo Sapiens
; TISSUE TYPE: Brain
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: -78...-1
; IDENTIFICATION METHOD: Von Heijne matrix
; OTHER INFORMATION: score 6.3
; OTHER INFORMATION: seq TLIMLLSWQLSVS/SV
US-08-905-223-411

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Query Match          14.0%; Score 99; DB 3; Length 80;
Best Local Similarity 58.8%; Pred. No. 0.00017;
Matches 20; Conservative 7; Mismatches 5; Indels 2; Gaps 1;

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Qy      49 VVDLLYWRDIKKTGVVFGASLFLLS--LTVFSI 80
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Db      47 VHDLIFWRDVKKTGFVFGTTLIMLLSWQLSVSSV 80

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RESULT 9
US-09-328-352-4866
; Sequence 4866, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 4866
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-4866

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Query Match          10.6%; Score 75; DB 4; Length 593;
Best Local Similarity 27.5%; Pred. No. 2.1;
Matches 25; Conservative 19; Mismatches 27; Indels 20; Gaps 5;

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Qy 55 WRDIKKT--GVVFGASLFLLLSLTVFSIV-----SVTAYIALALLSVTISFRIYKGVIA 107
 || :|:| | : | : : : || || :|:|:|: ||:|
 Db 258 WRGVKETWPAVLVGGGAFAIAQYLTSNFIGPELDPITAAIA-SLVSLTLLFRVWK----- 311

Qy 108 IAKSDEGHPFRAYLESEVAISEE--LVQKYS 136
 | || | : : : ||:|
 Db 312 -----PKHIFRFEPEAGQTLAQPTTVQRY 337

RESULT 10

US-08-853-659A-53

; Sequence 53, Application US/08853659A

; Patent No. 5925522

; GENERAL INFORMATION:

; APPLICANT: Wong, K.K.; Saffer, J.D.

; TITLE OF INVENTION: A Salmonella Sequence, Methods Of Detection

; TITLE OF INVENTION: Of A

; TITLE OF INVENTION: Salmonella Sequence, And Methods Of Detection Of
 Salmonella

; NUMBER OF SEQUENCES: 67

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Paul W. Zimmerman

; ADDRESSEE: Intellectual Property Services

; ADDRESSEE: Battelle Memorial Institute

; ADDRESSEE: PNNL P.O. Box 999

; STREET: Washington Way

; CITY: Richland

; STATE: Washington

; COUNTRY: U.S.A.

; ZIP: 99352

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette 3.50", 1.44 Mb storage

; COMPUTER: IBM PC/XT/AT

; OPERATING SYSTEM: MS-DOS

; SOFTWARE: Word Processor (WordPerfect 5.1)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/853,659A

; FILING DATE: Unknown

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: none

; FILING DATE: n/a

; INFORMATION FOR SEQ ID NO: 53:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 598 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

US-08-853-659A-53

Query Match 10.3%; Score 72.5; DB 2; Length 598;

Best Local Similarity 22.5%; Pred. No. 4.1;

Matches 25; Conservative 22; Mismatches 53; Indels 11; Gaps 2;

Qy 41 QKKHWKDKVVDLLYWRDIKKTGVVFGASLF-LLLSLTVFSIVSVTAYIALAL----- 91
 :|:| : : | : | : : : | : | : |

Db 149 KKKNGRSMSSAFVLWNEFQKIKPVLNLSIFQRIADIPIFIIFLIVIVNGLGVVIVPITM 208

Qy 92 --LSVTISFRIYKGVQAIKSDGHPFRAYLESEVAISEELVQKYSNSAL 140
 :|: || : : | || | ||| :| :: :| |
 Db 209 FIVSIIISLVNHHYTNELMNKQKEGQKNRNFISEVFLSIKMIHTLNNQGL 259

RESULT 11

US-08-366-783-5

; Sequence 5, Application US/08366783

; Patent No. 5650554

; GENERAL INFORMATION:

; APPLICANT: Moloney, Maurice M

; TITLE OF INVENTION: Oil-Body Proteins As Carriers Of

; TITLE OF INVENTION: High-Value Peptides In Plants

; NUMBER OF SEQUENCES: 22

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DEHLINGER & ASSOCIATES

; STREET: 350 CAMBRIDGE AVENUE, SUITE 250

; CITY: PALO ALTO

; STATE: California

; COUNTRY: United States

; ZIP: 94025-1536

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/366,783

; FILING DATE:

; CLASSIFICATION: 800

; ATTORNEY/AGENT INFORMATION:

; NAME: FABIAN, GARY

; REGISTRATION NUMBER: 33,875

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-324-0880

; TELEFAX: 415-324-0960

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 154 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-366-783-5

Query Match 10.1%; Score 71.5; DB 1; Length 154;

Best Local Similarity 26.2%; Pred. No. 0.83;

Matches 37; Conservative 16; Mismatches 49; Indels 39; Gaps 5;

Qy 33 RSWQEMDGQKKHWKDKVVDLLYWRDIKK--TGVVFGASLFLLLSLT----- 76

| :| |: : || | | | ||| :|||

Db 6 RDQYQMSGRGSDYSKS-----RQIAKAATAVTAGGSLLVLLSLTLVGTVIALTVATPL 58

Qy 77 --VFSIVSVTAYIALALL-----SVTISFRIYKG-VIQAIKSDGHPFRAY 120

:|| :| | | :||| ::|: ||| :|: ||: |

Db 59 LVIFSPILVPALITVALLITGFLSSGGFGIAAITVFSWIYKYLLEHPQGSCLKDSARMK 118

Qy	121	LESEVAISEELVQKYSNSALG	141
		: :	
Db	119	LGSKAQDLKDRAQYYGQQHTG	139

RESULT 12

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US-09-134-001C-4744
; Sequence 4744, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 4744
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4744

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Query Match 9.9%; Score 70; DB 4; Length 518;
Best Local Similarity 21.0%; Pred. No. 6.8;
Matches 21; Conservative 28; Mismatches 35; Indels 16; Gaps 4;

Qy	16	AVYSVSVGMH---NLLLLLEGRSWQEMDGQKKHWKDKVVDLLYWRDIKK----	TGVVFGAS	68
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Db	400	AIVAITIAWHPNDTILNLVGNWA---GFGAAFSPLVLVLSLYWKDLTRAGAI	SGMVAGAV	456
Qy	69	LFLLLSLTVFSIVSVTAYIAL-----ALLSVTISFRIYK		102
		: : : : : : : : : : : : :		
Db	457	VVIVWISWIKPLATINAFFGMYEIIPGFIVSVLITYIVSK		496

RESULT 13

US-09-422-936-79
; Sequence 79, Application US/09422936
; Patent No. 6465213
; GENERAL INFORMATION:
; APPLICANT: Ekstrand, Jonas
; TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES
; FILE REFERENCE: 06275-165002
; CURRENT APPLICATION NUMBER: US/09/422,936
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: US 09/242,608
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: PCT/SE98/01947
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: SWEDEN 9703914-2

; PRIOR FILING DATE: 1997-10-27
; PRIOR APPLICATION NUMBER: SWEDEN 9800864-2
; PRIOR FILING DATE: 1998-03-16
; PRIOR APPLICATION NUMBER: SWEDEN 9802575-2
; PRIOR FILING DATE: 1998-07-17
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 79
; LENGTH: 563
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-422-936-79

Query Match 9.9%; Score 70; DB 4; Length 563;
Best Local Similarity 28.3%; Pred. No. 7.6;
Matches 26; Conservative 13; Mismatches 35; Indels 18; Gaps 3;

Qy 30 LEGRSWQEMDGQKKHKWDKVVLLLYWRDIKKTGVVFGAS-----LFLLLSLTVFS 79
|:| |::: :| ||| || | | | |
Db 144 LQGSYKKGIG-----YYDSTKDDLWS---SKTDKWIGGSPPADQTLVIKTRFLSQKLF 195

Qy 80 IVSVTAYIALALLSVTISFRIYKGVIAIAKS 111
||| : : : | | : || || : : | |
Db 196 SVSVLSSLGIVLAVVCLSFNIYNHVRVYIQNS 227

RESULT 14

US-08-262-220-6

; Sequence 6, Application US/08262220
; Patent No. 6054296
; GENERAL INFORMATION:
; APPLICANT: BERGSTROM SVEN
; APPLICANT: BARBOUR ALAN G.
; TITLE OF INVENTION: NEW 66 KDA ANTIGEN FROM BORRELIA
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 SEVENTH STREET, N.W.
; CITY: WASHINGTON
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/262,220
; FILING DATE: 20-JUN-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: COOPER, IVER P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: BERGSTROM=3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528

; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 619 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-262-220-6

Query Match 9.9%; Score 70; DB 3; Length 619;
Best Local Similarity 39.0%; Pred. No. 8.7;
Matches 16; Conservative 6; Mismatches 15; Indels 4; Gaps 1;

Qy 32 GRSWQEMDGQKKHWKDKVVD----LLYWRDIKKTGVVFGAS 68
| : | : || : || | | : || : || | |
Db 384 GLAWNKDDGEKESWKVKGSDSYSTRLFGEQDKKSGVALGIS 424

RESULT 15

US-08-471-733-6

; Sequence 6, Application US/08471733
; Patent No. 6068842
; GENERAL INFORMATION:
; APPLICANT: BERGSTROM SVEN
; APPLICANT: BARBOUR ALAN G.
; TITLE OF INVENTION: NEW 66 KDA ANTIGEN FROM BORRELIA
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 SEVENTH STREET, N.W.
; CITY: WASHINGTON
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,733
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/262,220
; FILING DATE: 20-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: COOPER, IVER P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: BERGSTROM=3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE STICS: No. 1. ;175X
; LENGTH: 619 amino acids
; TYPE: amino acid

; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-471-733-6

Query Match 9.9%; Score 70; DB 3; Length 619;
Best Local Similarity 39.0%; Pred. No. 8.7;
Matches 16; Conservative 6; Mismatches 15; Indels 4; Gaps 1;

Qy 32 GRSWQEMDGQKKHWKDKVVD----LLYWRDIKKTGVVFGAS 68
| : | : ||:|: || | | : ||:| | |
Db 384 GLAWNKDDGEKESWKVGSDSYSTRLFGEQDKKSGVALGIS 424

Search completed: January 22, 2004, 16:34:54
Job time : 3.42077 secs

OM protein - protein search, using sw model

Run on: January 22, 2004, 16:31:15 ; Search time 3.84837 Seconds
(without alignments)
3523.514 Million-cell updates/sec

Title: US-09-830-972-32
Perfect score: 705
Sequence: 1 QASGEAGVSCLRENFAVYSV.....ESEVAISEELVQKYSNSALG 141

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query	Match Length			
1	349	49.5	208	2	I60904	neuroendocrine-spe
2	348	49.4	267	2	A60021	tropomyosin-relate
3	337	47.8	776	2	A46583	neuroendocrine-spe
4	162	23.0	2484	2	T26216	hypothetical prote
5	159	22.6	2607	2	T26215	hypothetical prote
6	158	22.4	222	2	T26213	hypothetical prote
7	83.5	11.8	295	2	S59439	probable membrane
8	81.5	11.6	464	2	C88188	protein C18H9.5 [i
9	79	11.2	618	2	T24228	hypothetical prote
10	78.5	11.1	458	2	A72258	hypothetical prote
11	77.5	11.0	261	2	F64924	probable thiosulfa
12	77.5	11.0	583	2	T49359	hypothetical prote
13	76.5	10.9	481	2	C95920	hypothetical membr

14	75.5	10.7	545	2	F64665	glucose-6-phosphat
15	74.5	10.6	545	2	E71851	glucose-6-phosphat
16	74	10.5	268	2	F64024	hypothetical prote
17	73	10.4	393	2	S67763	probable membrane
18	73	10.4	888	2	T01081	hypothetical prote
19	72.5	10.3	278	2	AD0147	probable ABC trans
20	72.5	10.3	302	2	AE2863	conserved hypothet
21	72.5	10.3	302	2	D97640	hypothetical prote
22	72.5	10.3	417	2	B96977	probable Mn transp
23	72.5	10.3	598	2	T14886	leukotoxin express
24	72	10.2	271	2	T13013	hypothetical prote
25	72	10.2	299	2	B69155	hypothetical prote
26	72	10.2	1783	2	T42386	unconventional myo
27	72	10.2	3511	2	A59295	unconventional myo
28	71.5	10.1	255	2	E84899	hypothetical prote
29	71.5	10.1	537	2	G82873	conserved hypothet
30	71	10.1	346	1	WMVZ1W	3beta-hydroxy-Delt
31	71	10.1	346	1	WMVZ2W	3beta-hydroxy-Delt
32	71	10.1	346	2	T37430	hydroxysteroid deh
33	71	10.1	476	2	B97096	2-oxoglutarate/mal
34	71	10.1	1065	2	T25068	hypothetical prote
35	70.5	10.0	153	2	AB3226	conserved hypothet
36	70.5	10.0	261	2	A90926	hypothetical prote
37	70.5	10.0	261	2	E85774	hypothetical prote
38	70.5	10.0	291	2	B69098	phosphate transpor
39	70	9.9	271	2	AC1320	hypothetical prote
40	70	9.9	619	2	S55502	membrane-associate
41	70	9.9	737	2	AE1678	heavy metal-transp
42	69.5	9.9	188	2	T04714	hypothetical prote
43	69.5	9.9	403	2	T04821	hypothetical prote
44	69.5	9.9	415	2	D95248	conserved hypothet
45	69.5	9.9	504	2	E83898	spore germination

ALIGNMENTS

RESULT 1

I60904

neuroendocrine-specific protein C - human

C;Species: Homo sapiens (man)

C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 05-Nov-1999

C;Accession: I60904

R;Roebroek, A.J.; van de Velde, H.J.; Van Bokhoven, A.; Broers, J.L.; Ramaekers, F.C.; Van de Ven, W.J.

J. Biol. Chem. 268, 13439-13447, 1993

A;Title: Cloning and expression of alternative transcripts of a novel neuroendocrine-specific gene and identification of its 135-kDa translational product.

A;Reference number: A46583; MUID:93293865; PMID:7685762

A;Accession: I60904

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-208 <RES>

A;Cross-references: GB:L10335; NID:g307310; PIDN:AAA59952.1; PID:g307311

C;Genetics:

A;Gene: GDB:RTN1; NSP

A;Cross-references: GDB:203968; OMIM:600865
A;Map position: 14q21-14q22

Query Match 49.5%; Score 349; DB 2; Length 208;
Best Local Similarity 63.4%; Pred. No. 5e-28;
Matches 64; Conservative 19; Mismatches 18; Indels 0; Gaps 0;

```
Qy      37 EMDGQKKHKWVKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTI 96
      :|| :|| : :|||||||:|:|:|:| : || ||| ||:| || || ||
Db      9 KMDCVWSNWKSAIDLLYWRDIKQTGIVFGSFLLLLFSLTQFSVSVVAYLALAALSATI 68

Qy      97 SFRIYKGVIAIAKSDEGHPPFRAYLESEVAISEELVQKYSN 137
      ||||| |:|:| |:|||||:|||| |: :|:| :|||:
Db      69 SFRIYKSVLQAVQKTDEGHPPFKAYLELEITLSQEQIQKYTD 109
```

RESULT 2

A60021

tropomyosin-related protein, neuronal - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 05-Nov-1999

C;Accession: A60021

R;Wieczorek, D.F.; Hughes, S.R.

Brain Res. Mol. Brain Res. 10, 33-41, 1991

A;Title: Developmentally regulated cDNA expressed exclusively in neural tissue.

A;Reference number: A60021; MUID:91278684; PMID:1647480

A;Accession: A60021

A;Molecule type: mRNA

A;Residues: 1-267 <WIE>

A;Cross-references: EMBL:X52817; NID:g456549; PIDN:CAA37001.1; PID:g456550

C;Comment: This neuronal-specific mRNA was identified by hybridization to an alpha-tropomyosin probe but does not show homology in amino acid sequence.

Query Match 49.4%; Score 348; DB 2; Length 267;
Best Local Similarity 64.0%; Pred. No. 8.4e-28;
Matches 64; Conservative 18; Mismatches 18; Indels 0; Gaps 0;

```
Qy      38 MDGQKKHKWVKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS 97
      || :|| : :|||||||:|:|:|:| : || ||| ||:| || || ||
Db      1 MDCVWSNWKSAIDLLYWRDIKQTGIVFGSFLLLLFSLTQFSVSVVAYLALAALSATIS 60

Qy      98 FRIYKGVIAIAKSDEGHPPFRAYLESEVAISEELVQKYSN 137
      ||||| |:|:| |:|||||:|||| |: :|:| :|||:
Db      61 FRIYKSVLQAVQKTDEGHPPFKAYLELEITLSQEQIQKYTD 100
```

RESULT 3

A46583

neuroendocrine-specific protein, splice form A - human

N;Contains: neuroendocrine-specific protein, splice form B

C;Species: Homo sapiens (man)

C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 05-Nov-1999

C;Accession: A46583; I60903

R;Roebroek, A.J.; van de Velde, H.J.; Van Bokhoven, A.; Broers, J.L.; Ramaekers, F.C.; Van de Ven, W.J.

J. Biol. Chem. 268, 13439-13447, 1993

A;Title: Cloning and expression of alternative transcripts of a novel neuroendocrine-specific gene and identification of its 135-kDa translational product.

A;Reference number: A46583; MUID:93293865; PMID:7685762

A;Accession: A46583

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-776 <ROE1>

A;Cross-references: GB:L10333; NID:g307306; PIDN:AAA59950.1; PID:g307307

A;Accession: I60903

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 421-776 <ROE2>

A;Cross-references: GB:L10334; NID:g307308; PIDN:AAA59951.1; PID:g307309

C;Genetics:

A;Gene: GDB:RTN1; NSP

A;Cross-references: GDB:203968; OMIM:600865

A;Map position: 14q21-14q22

Query Match 47.8%; Score 337; DB 2; Length 776;
Best Local Similarity 67.4%; Pred. No. 3.5e-26;
Matches 62; Conservative 16; Mismatches 14; Indels 0; Gaps 0;

Qy 46 KDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV 105
| | : ||||| ||| : ||| : | | | | | : ||| || : ||| | | ||||| | :
Db 586 KQKAIDLLYWRDIKQTGIVFGSFLLLFSLTQFSVSVVAYLALAALSATISFRIYKSVL 645

Qy 106 QAIKSDEGHPPFRAYLESEVAISEELVQKYSN 137
|| : | : ||||| : ||| | : : | : | : ||| : :
Db 646 QAVQKTDEGHPPFKAYLELEITLSQEIQKYTD 677

RESULT 4

T26216

hypothetical protein W06A7.3c - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C;Accession: T26216

R;Ainscough, R.

submitted to the EMBL Data Library, August 1996

A;Reference number: Z20173

A;Accession: T26216

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-2484 <WIL>

A;Cross-references: EMBL:Z78066; PIDN:CAB51467.1; GSPDB:GN00023; CESP:W06A7.3c

A;Experimental source: clone W06A7

C;Genetics:

A;Gene: CESP:W06A7.3c

A;Map position: 5

A;Introns: 1827/1; 1866/3; 1963/3; 1990/3; 2262/1; 2289/1; 2339/2; 2463/2

Query Match 23.0%; Score 162; DB 2; Length 2484;
Best Local Similarity 31.5%; Pred. No. 7.7e-08;
Matches 34; Conservative 22; Mismatches 48; Indels 4; Gaps 1;

Qy 25 HNLLLLLEGRSWQEMDGQKKHWKDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVT 84

Db 2269 HSILKHHGDAWIDF---KTVPPCVLDVIYWRDAKKSATVLSLALLVLFVLAKYPLLTVV 2324
 QY 85 AYIALALLSVTISFRYIKGVIQAIKSDGHPFRAYLESEVAISEELV 132
 Db 2325 TYSLLLALGAAAGFRVFKKVEAOIKKTDSEHPFSEILAODLTLPOEKV 2372

RESULT 5

T26215
hypothetical protein W06A7.3a - *Caenorhabditis elegans*
C;Species: *Caenorhabditis elegans*
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T26215
R;Ainscough, R.
submitted to the EMBL Data Library, August 1996
A;Reference number: Z20173
A;Accession: T26215
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-2607 <WIL>
A;Cross-references: EMBL:Z78066; PIDN:CAB01522.2; GSPDB:GN00023; CESP:W06A7.3a
A;Experimental source: clone W06A7
C;Genetics:
A;Gene: CESP:W06A7.3a
A;Map position: 5
A;Introns: 1827/1; 1866/3; 1963/3; 1990/3; 2262/1; 2289/1; 2412/1; 2462/2;
2586/2

Query Match 22.6%; Score 159; DB 2; Length 2607;
Best Local Similarity 34.5%; Pred. No. 1.6e-07;
Matches 30; Conservative 19; Mismatches 38; Indels 0; Gaps 0;

```
Qy      46 KDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI 105  
        | :|:|::||| ||: :|   :| :| | : ::| | | | ||::| |  
Db     2409 KKEVLDDVIYWRDAKKSIAIVLSLALLVLFVLAKYPLLTVVVTYSLLLLALGAAAGFRVFVKVE 2468  
  
Qy      106 QAIKSDEGHPPFRAYLESEVAISEELV 132  
        | |:| ||| . | :: : :| |  
Db     2469 AOIKKTDSEHPFSEILAODLTLPOEKV 2495
```

RESULT 6

T26213
hypothetical protein W06A7.3b - *Caenorhabditis elegans*
C;Species: *Caenorhabditis elegans*
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T26213
R;Ainscough, R.
submitted to the EMBL Data Library, August 1996
A;Reference number: Z20173
A;Accession: T26213
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-222 <WIL>
A;Cross-references: EMBL:Z78066; PIDN:CAB01523.1; GSPDB:GN00023; CESP:W06A7.3b
A;Experimental source: clone W06A7

C;Genetics:
A;Gene: CESP:W06A7.3b
A;Map position: 5
A;Introns: 27/1; 77/2; 201/2

Query Match 22.4%; Score 158; DB 2; Length 222;
Best Local Similarity 34.1%; Pred. No. 1.4e-08;
Matches 29; Conservative 19; Mismatches 37; Indels 0; Gaps 0;

```
Qy      48 KVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIIQA 107
          |::|::| || | |::| :| :| | :::| | | | |::| |
Db      26 KILDVIYWRDAKKSIVLSLALLVFLVLAKEYPLLVVTYSLLLALGAAAGFRVFKKVEAQ 85

Qy      108 IAKSDEGHPFRAYLESEVAISEELV 132
          | |::| || | | : : : | |
Db      86 IKKTDSEHPFSEILAQDLTLPQEKV 110
```

RESULT 7

S59439
probable membrane protein YDR233c - yeast (*Saccharomyces cerevisiae*)
N;Alternate names: hypothetical protein YD9934.17c
C;Species: *Saccharomyces cerevisiae*
C;Date: 30-Nov-1995 #sequence_revision 16-Feb-1996 #text_change 19-Apr-2002
C;Accession: S59439
R;Murphy, L.; Harris, D.
submitted to the EMBL Data Library, March 1995
A;Reference number: S59423
A;Accession: S59439
A;Molecule type: DNA
A;Residues: 1-295 <MUR>
A;Cross-references: EMBL:Z48612; NID:g728671; PID:g728688; GSPDB:GN00004;
MIPS:YDR233c
A;Experimental source: strain AB972
C;Genetics:
A;Gene: MIPS:YDR233c
A;Cross-references: SGD:S0002641
A;Map position: 4R
C;Keywords: transmembrane protein
F;40-56/Domain: transmembrane #status predicted <TM1>
F;146-162/Domain: transmembrane #status predicted <TM2>

Query Match 11.8%; Score 83.5; DB 2; Length 295;
Best Local Similarity 26.3%; Pred. No. 0.72;
Matches 25; Conservative 17; Mismatches 32; Indels 21; Gaps 2;

```
Qy      41 QKKHWDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRI 100
          |::| | | | |::| :|| || | | | ::: :| :| |
Db      12 QQQQQKSCNCDLLLWRNPVQTGKYFGGSLLALLILKKVNLITFFLKVAYTILFTT----- 66

Qy      101 YKGVIIQAIKSDEGHPFRAYLESEVAISEELVQKY 135
          | |::| | : : : | : |
Db      67 --GSIEFVSK-----LFLGQGLITKY 85
```

RESULT 8
C88188

protein C18H9.5 [imported] - *Caenorhabditis elegans*
 C;Species: *Caenorhabditis elegans*
 C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
 C;Accession: C88188
 R;anonymous, The C. elegans Sequencing Consortium.
 Science 282, 2012-2018, 1998
 A;Title: Genome sequence of the nematode C. elegans: a platform for
 investigating biology.
 A;Reference number: A75000; MUID:99069613; PMID:9851916
 A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and
 www.sanger.ac.uk/Projects/C_elegans/ for a list of authors
 A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103,
 1999; and Science 285, 1493, 1999
 A;Accession: C88188
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-464 <STO>
 A;Cross-references: GB:chr_II; PID:g722384; GSPDB:GN00020; CESP:C18H9.5
 C;Genetics:
 A;Gene: C18H9.5
 A;Map position: 2

Query Match 11.6%; Score 81.5; DB 2; Length 464;
 Best Local Similarity 25.9%; Pred. No. 1.9;
 Matches 38; Conservative 28; Mismatches 50; Indels 31; Gaps 8;

```

Qy      8 VSCLRENFAVYSVSVGMHNLLEGRSWQEMDGQKKHWKDKVVDLLYWRDIKKTGVVFG- 66
      ::| | : : :| | ::| :| : | | :| |
Db     41 ITCTNANMILMNFTVICMNDVIEQKSF---SNQTHWLEKSSDISLTFSAAAVGAIFGT 96

Qy     67 ASLFLLLS-----LTVFSIVSV--TAYIALA----LLSVTISFRIYKGV-----I 105
      |:| | | : :| | : | | :| | :| :| :| |
Db     97 VPAVTLISKYGIRKVLTVYGLLSAGGTLMLPLAVNYGLIPVLIA-RLFQGVGASILYSSI 155

Qy    106 QAIKS----DEGHPFRAYLESEVAIS 128
      |:| :| | | | |
Db    156 GTISESWSPINEIGTFVAFLLSSAFQIS 182

```

RESULT 9

T24228

hypothetical protein R166.2 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C;Accession: T24228

R;Matthews, P.

submitted to the EMBL Data Library, August 1995

A;Reference number: Z19859

A;Accession: T24228

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-618 <WIL>

A;Cross-references: EMBL:Z50795; PIDN:CAA90663.1; GSPDB:GN00020; CESP:R166.2

A;Experimental source: clone R166

C;Genetics:

A;Gene: CESP:R166.2

A;Map position: 2

Query Match 11.2%; Score 79; DB 2; Length 618;
Best Local Similarity 29.1%; Pred. No. 4.6;
Matches 32; Conservative 22; Mismatches 32; Indels 24; Gaps 6;

RESULT 10

hypothetical protein - *Thermotoga maritima* (strain MSB8)

C;Date: 11-Jun-1999 #sequence revision 11-Jun-1999 #text change 21-Jul-2000

R.; Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, E.K.; Peterson, J.D.; Nelson, W.C.; Ketchum, K.A.; McDonald, L.; Utterback, T.R.; Malek, J.A.; Linher, K.D.; Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.; Heidelberg, J.; Sutton, G.G.; Fleischmann, R.D.; White, O.; Salzberg, S.L.; Smith, H.O.; Venter, J.C.; Fraser, C.M.

A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome sequence of *Thermotoga maritima*.

A;Accession: A72258

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-458 <ARN>

A;Cross-references: GB:AE001793; GB:AE000512; NID:g4981963; PIDN:AAD36479.1;
PID:g4981972; TIGR:TM1408

A; Experimental source: strain MSB8

C;Genetics:

A;Gene: TM1408

QY 14 NFAVY-----SVSVGMHNLLLLLEGRSWQEMDGQKKH-----WKD 47
 || : | : | || : || ||
 Db 196 NFLILSYLRSSIRIGFDFLL-----TRKHPQLLFIFYFYLSIWIDNFIWKV 244

QY 48 KVDLL-----YWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFR 99
| :: | | | | | | : | | | : | | : |
Db 245 KGIEIAPGFFMSPEY--DI PK---FMASLFFIPSLVVFN-----LSMETVFQR 287

Qy 100 IYKGVIAIAKSDEGHPPFRAYLESEVAISEELVQKYSN 137
 |||::|:| ||: || |: :| | :||
 Db 288 NYKGLMQSIV-SDK--PMRVI SENLKKLSLSLRHAFSN 322

F64924

C;Species: Escherichia coli

C;Accession: F64924

A;Title: The complete genome sequence of Escherichia coli K-12.

A:Accession: F64924

A;Molecule type: DNA

A; Cross-references: GB:AE000262; GB:U00096; NID:g1787955; PIDN:AAC74740.1;

A;Experimental source: strain K-12, substrain MG1655

C;Keywords: sulfurtransferase; transmembrane protein

F;83-99/Domain: transmembrane #status predicted <TM02>

F:112-128/Domain: transmembrane #status predicted <TM03>

F:187-203/Domain: transmembrane #status predicted <TM04>

F;224-240/Domain: transmembrane #status predicted <TM05>

Query Match 11.0%; Score 77.5; DB 2; Length 261;
Best Local Similarity 27.6%; Pred. No. 2.6;
Matches 29; Conservative 16; Mismatches 43; Indels 17; Gaps 4;

Qy 22 VGMHNLLLLLEGRSWQEMD-GQKKHWKDKVVDLLYWRDIKKTGVVFGASLFLLL---SLT 76
 :|:| || | | :| : | | :| : | | :| :
 Db 44 LGLHALLRARGVKKSATDHGEKIYLYSKAVRLWHWSN-----ALLFVILLASGLIN 94

Qy 77 VFSIVSVTAYIALALLSVTISFRI---YKGVIQAIKASDEGHPFR 118
|::| || :| : | : | : | | || :|
Db 95 HFAMVGATAVKSLVAVHEVCGFLLACWLGFVLINAVGDNGHHYR 139

T49359

C;Species: Neurospora crassa

C;Accession: T49359

submitted to the Protein Sequence Database, May 2000

A;Reference number: Z25022

A;Accession: T49359

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-583 <SCH>

A;Cross-references: EMBL:AL355927; GSPDB:GN00116; NCSP:B1D1.130

A;Experimental source: BAC clone B1D1; strain OR74A
C;Genetics:
A;Gene: NCSP:B1D1.130
A;Map position: 6
A;Introns: 44/1

Query Match 11.0%; Score 77.5; DB 2; Length 583;
Best Local Similarity 27.5%; Pred. No. 6.1;
Matches 28; Conservative 13; Mismatches 28; Indels 33; Gaps 4;

```
Qy      52 LLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIAKS 111
      | | | : : : : | | | | | | : | | : | | : | | :
Db      67 LCYW-PLERRLLVLHALLLLLLLSLEHYS-----AYTRVLLHITSSINL----- 109

Qy      112 DEGHPFRAYLESEVAIS-----EELVQKYSNSALG 141
      | | : : | | : : | | : | | |
Db      110 ----PLRVLVDDEVVAKAIAWMAKDINPEELIQKRIEECAG 147
```

RESULT 13

C95920

hypothetical membrane protein [imported] - *Sinorhizobium meliloti* (strain 1021)
megaplasmid pSymB

C;Species: *Sinorhizobium meliloti*

C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001

C;Accession: C95920

R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernandez-Lucas, I.; Becker, A.; Cowie, A.; Gouzy, J.; Golding, B.; Puhler, A.

Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001

A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N₂-fixing endosymbiont *Sinorhizobium meliloti*.

A;Reference number: A95842; MUID:21396508; PMID:11481431

A;Accession: C95920

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-481 <KUR>

A;Cross-references: GB:AL591985; PIDN:CAC49027.1; PID:gl5140512; GSPDB:GN00167

A;Experimental source: strain 1021, megaplasmid pSymB

R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, F.; Barnett, M.J.; Becker, A.; Boistard, P.; Bothe, G.; Boutry, M.; Bowser, L.; Buhrmester, J.; Cadieu, E.; Capela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; Gloux, S.; Godrie, T.; Goffeau, A.; Golding, B.; Gouzy, J.; Gurjal, M.; Hernandez-Lucas, I.; Hong, A.; Huizar, L.; Hyman, R.W.; Jones, T.

Science 293, 668-672, 2001

A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, V.; Masuy, D.; Palm, C.; Peck, M.C.; Pohl, T.M.; Portetelle, D.; Purnelle, B.; Ramsperger, U.; Surzycki, R.; Thebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.C.; Batut, J.

A;Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*.

A;Reference number: A96039; MUID:21368234; PMID:11474104

A;Contents: annotation

C;Genetics:

A;Gene: Smb21048

A;Genome: plasmid

Query Match 10.9%; Score 76.5; DB 2; Length 481;
Best Local Similarity 37.7%; Pred. No. 6.3;
Matches 23; Conservative 8; Mismatches 27; Indels 3; Gaps 2;

```
Qy      53 LYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIAKSD 112
      :||| | | | |||| | : | || ||: ||: ||: :: | : |
Db      238 VYWRKTKSR--VAQALAFLLLVLLLLSTSSV-AYVGLAVLSIPVALSISWSFSLSGRMDKD 294

Qy      113 E 113
      |
Db      295 E 295
```

RESULT 14

F64665

glucose-6-phosphate isomerase (EC 5.3.1.9) - *Helicobacter pylori* (strain 26695)

C;Species: *Helicobacter pylori*

C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 16-Jul-1999

C;Accession: F64665

R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.;
Fleischmann, R.D.; Ketchum, K.A.; Klenk, H.P.; Gill, S.; Dougherty, B.A.;
Nelson, K.; Quackenbush, J.; Zhou, L.; Kirkness, E.F.; Peterson, S.; Loftus, B.;
Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenney, K.; Fitzgerald,
L.M.; Lee, N.; Adams, M.D.; Hickey, E.K.; Berg, D.E.; Gocayne, J.D.; Utterback,
T.R.; Peterson, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.;
Bowman, C.; Watthey, L.

Nature 388, 539-547, 1997

A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.;

Fraser, C.M.; Venter, J.C.

A;Title: The complete genome sequence of the gastric pathogen *Helicobacter pylori*.

A;Reference number: A64520; MUID:97394467; PMID:9252185

A;Accession: F64665

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-545 <TOM>

A;Cross-references: GB:AE000622; GB:AE000511; NID:g2314317; PIDN:AAD08211.1;

PID:g2314323; TIGR:HP1166

C;Superfamily: glucose-6-phosphate isomerase

C;Keywords: intramolecular oxidoreductase; isomerase

Query Match 10.7%; Score 75.5; DB 2; Length 545;
Best Local Similarity 25.3%; Pred. No. 9.1;
Matches 37; Conservative 20; Mismatches 44; Indels 45; Gaps 6;

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Qy      23 GMHNLL-----LLEGRSWQEMDQ---KKHWKDKVVDLLYWRDIKKTGVVFGASL 69
      | | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      411 GHHEILFSNVLAQAQAFMKGKSYEEALGELLFKGLDKDEAKDLAHR-----VFFGNRP 464

Qy      70 FLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIAKSD----- 112
      : | | | : : | : | | : : : ||| | | |
Db      465 SNILLLEKISPSNIGALVALYEHKVFFV-----QGVWDINSFDQWGVELGKELAVPILQE 519

Qy      113 -EGHPFRAYLESEVAISEELVQKYSN 137
      ||| || : | : : | : | |
Db      520 LEGHKSNAFYDSS---TKHLIELYKN 542
```

RESULT 15

E71851

glucose-6-phosphate isomerase - *Helicobacter pylori* (strain J99)

C;Species: *Helicobacter pylori*

A;Variety: strain J99

C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 16-Jul-1999

C;Accession: E71851

R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.;
Smith, D.R.; Noonan, B.; Guild, B.C.; deJonge, B.L.; Carmel, G.; Tummino, P.J.;
Caruso, A.; Uria-Nickelsen, M.; Mills, D.M.; Ives, C.; Gibson, R.; Merberg, D.;
Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Trust, T.J.

Nature 397, 176-180, 1999

A;Title: Genomic sequence comparison of two unrelated isolates of the human
gastric pathogen *Helicobacter pylori*.

A;Reference number: A71800; MUID:99120557; PMID:9923682

A;Accession: E71851

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-545 <ARN>

A;Cross-references: GB:AE001536; GB:AE001439; NID:g4155675; PIDN:AAD06664.1;

PID:g4155679

A;Experimental source: strain J99

C;Genetics:

A;Gene: *pgi*

C;Superfamily: glucose-6-phosphate isomerase

Query Match 10.6%; Score 74.5; DB 2; Length 545;
Best Local Similarity 25.3%; Pred. No. 12;
Matches 37; Conservative 19; Mismatches 45; Indels 45; Gaps 6;

```

Qy      23 GMHNLL-----LLEGRSWQEMDQ---KKHWKDKVVDLLYWRDIKKTGVVFGASL 69
      | | : |          ::|:|::| | : |   | | : |   | |
Db      411 GHHEILFSNVLAQAQAFMKGKSYEEALGELLSKGLDKDEAKDLAHR-----VFFGNRP 464

Qy      70 FLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIAKSD----- 112
      : | | | : : | : | | | :   : | | | | |
Db      465 SNILLEKISPSNIGALVALYEHKVFV----QGVIWDINSFDQWGVELGKELAVPILQE 519

Qy     113 -EGHPFRAYLESEVAISEELVQKYSN 137
      | | |   | | : |   : | : | |
Db     520 LEGHKSNA YFDSS---TRHLIELYKN 542

```

Search completed: January 22, 2004, 16:33:08

Job time : 15.8484 secs

OM protein - protein search, using sw model

Run on: January 22, 2004, 16:31:15 ; Search time 7.37604 Seconds
(without alignments)
4932.919 Million cell updates/sec

Title: US-09-830-972-32
Perfect score: 705
Sequence: 1 QASGEAGVSLRENFAVYSV.....ESEVAISEELVQKYSNSALG 141

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp Vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_cheap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query				
No.	Score	Mp1450Xongth	DB	ID	rm R	Description

1	447	63.4	639	11	Q8K290	Q8k290 mus musculu
2	447	63.4	986	4	Q8IUA4	Q8iua4 homo sapien
3	447	63.4	1046	11	Q8BGK7	Q8bgk7 mus musculu
4	447	63.4	1162	11	Q8BGM9	Q8bgm9 mus musculu
5	443	62.8	356	11	Q8BH78	Q8bh78 mus musculu
6	443	62.8	375	11	Q8BHF5	Q8bhf5 mus musculu
7	443	62.8	392	4	Q96B16	Q96b16 homo sapien
8	436.5	61.9	1163	11	Q8K3G8	Q8k3g8 mus musculu
9	432.5	61.3	357	11	Q8K3G7	Q8k3g7 mus musculu
10	386	54.8	179	6	Q9GM33	Q9gm33 macaca fasc
11	348	49.4	199	4	Q9BQ59	Q9bq59 homo sapien
12	348	49.4	267	11	Q63765	Q63765 rattus sp.
13	337	47.8	780	11	Q8K4S4	Q8k4s4 mus musculu
14	337	47.8	780	11	Q8K0T0	Q8k0t0 mus musculu
15	325	46.1	208	13	Q90637	Q90637 gallus gall
16	320	45.4	760	13	Q90638	Q90638 gallus gall
17	308	43.7	236	11	Q8VBU0	Q8vbu0 rattus norv
18	308	43.7	237	11	Q8C6D5	Q8c6d5 mus musculu
19	308	43.7	643	11	Q8CCU2	Q8ccu2 mus musculu
20	255	36.2	234	5	Q9VMW3	Q9vmw3 drosophila
21	253	35.9	224	5	Q9VMW1	Q9vmw1 drosophila
22	252	35.7	222	5	Q9VMW4	Q9vmw4 drosophila
23	252	35.7	595	5	Q9VMV9	Q9vmv9 drosophila
24	250	35.5	202	5	Q9VMW2	Q9vmw2 drosophila
25	162	23.0	2484	5	Q9U347	Q9u347 caenorhabdi
26	159	22.6	2607	5	Q23187	Q23187 caenorhabdi
27	158	22.4	222	5	Q23188	Q23188 caenorhabdi
28	102.5	14.5	154	5	Q9VIB7	Q9vib7 drosophila
29	102.5	14.5	158	5	Q24199	Q24199 drosophila
30	85	12.1	457	10	Q8LDS3	Q8lds3 arabidopsis
31	83.5	11.8	295	3	Q04947	Q04947 saccharomyc
32	81.5	11.6	464	5	Q09484	Q09484 caenorhabdi
33	80	11.3	564	10	Q8L7Z9	Q8l7z9 spinacia ol
34	79	11.2	568	16	Q9CKM1	Q9ckm1 pasteurella
35	79	11.2	618	5	Q22003	Q22003 caenorhabdi
36	78.5	11.1	458	16	Q9X1C8	Q9x1c8 thermotoga
37	77.5	11.0	243	11	Q9JKA2	Q9jka2 mus musculu
38	77.5	11.0	798	3	Q9P6A7	Q9p6a7 neurospora
39	77	10.9	563	10	Q8L801	Q8l801 sorghum bic
40	76.5	10.9	481	16	Q92VS2	Q92vs2 rhizobium m
41	76.5	10.9	582	13	Q8AXT5	Q8axt5 salmo salar
42	76	10.8	563	10	Q9FMF7	Q9fmf7 arabidopsis
43	75.5	10.7	246	11	Q9JKA0	Q9jka0 mus musculu
44	75	10.6	255	10	Q9SH59	Q9sh59 arabidopsis
45	74.5	10.6	294	16	Q8D716	Q8d716 vibrio vuln

ALIGNMENTS

RESULT 1

Q8K290

ID	Q8K290	PRELIMINARY;	PRT;	639 AA.
AC	Q8K290;			
DT	01-OCT-2002	(TrEMBLrel. 22, Created)		
DT	01-OCT-2002	(TrEMBLrel. 22, Last sequence update)		
DT	01-MAR-2003	(TrEMBLrel. 23, Last annotation update)		


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RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=22376540; PubMed=12488097;
RA Oertle T., van der Putten H., Schwab M.E.;
RT "Genomic Structure and Functional Characterization of the Promoter
RT Structures of Human and Mouse Nogo/Rtn-4.";
RL J. Mol. Biol. 325:299-323(2003).
DR EMBL; AY102285; AAM64244.1; -.
DR EMBL; AY123245; AAM64249.1; -.
DR EMBL; AY123246; AAM64250.1; -.
DR EMBL; AY123247; AAM64251.1; -.
DR EMBL; AY123248; AAM64252.1; -.
DR EMBL; AY123249; AAM64253.1; -.
DR EMBL; AY123250; AAM64254.1; -.
SQ SEQUENCE 986 AA; 108449 MW; 0CDE8F647036415A CRC64;

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RESULT 3

```

ID      Q8BGK7          PRELIMINARY;          PRT;   1046 AA.
AC      Q8BGK7;
DT      01-MAR-2003 (TrEMBLrel. 23, Created)
DT      01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT      01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE      RTN4.
GN      RTN4.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=129/SvcJ7, and 129SvcJ7;
RA      Oertle T., van der Putten H., Schwab M.E.;
RT      "Genomic Structure and Functional Characterization of the Promoter
RT      Structures of Human and Mouse Nogo/Rtn-4.";
RL      Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN=129/SvcJ7, and 129SvcJ7;
RA      Oertle T., Schwab M.E.;
RL      Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN      [3]

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RP SEQUENCE FROM N.A.
 RC STRAIN=129/SvcJ7;
 RA Van der Putten H.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129SvcJ7;
 RA Van der Putten H., Mir A.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AY102280; AAM73502.1; -.
 DR EMBL; AY102286; AAM73507.1; -.
 SQ SEQUENCE 1046 AA; 114221 MW; 8CE2E2238ED51222 CRC64;

Query Match 63.4%; Score 447; DB 11; Length 1046;
 Best Local Similarity 96.9%; Pred. No. 8.6e-37;
 Matches 93; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 46 KDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGI 105
 | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 856 KTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGI 915
 Qy 106 QAIKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141
 ||| ||||||||||||||||||||||||||||||||
 Db 916 QAIKSDEGHPFRAYLESEVAISEELVQKYSNSALG 951

RESULT 4

Q8BGM9

ID Q8BGM9 PRELIMINARY; PRT; 1162 AA.
 AC Q8BGM9;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE RTN4.
 GN RTN4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SvcJ7, and 129SvcJ7;
 RA Oertle T., van der Putten H., Schwab M.E.;
 RT "Genomic Structure and Functional Characterization of the Promoter
 RT Structures of Human and Mouse Nogo/Rtn-4.";
 RL Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SvcJ7, and 129SvcJ7;
 RA Oertle T., Schwab M.E.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SvcJ7;
 RA Van der Putten H.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
 RN [4]

RP SEQUENCE FROM N.A.
RC STRAIN=129SvcJ7;
RA Van der Putten H., Mir A.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY102284; AAM73506.1; -.
DR EMBL; AY102286; AAM73511.1; -.
SQ SEQUENCE 1162 AA; 126613 MW; 855697FBEE11781F CRC64;

Query Match 63.4%; Score 447; DB 11; Length 1162;
Best Local Similarity 96.9%; Pred. No. 9.6e-37;
Matches 93; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

[illegible]

RESULT 5

08BH78

```

ID      P8BH78          PRELIMINARY;          PRT;      356 AA.
AC      Q8BH78;
DT      01-MAR-2003 (TrEMBLrel. 23, Created)
DT      01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT      01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE      RTN4.
GN      RTN4.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=129/SvcJ7, and 129SvcJ7;
RA      Oertle T., van der Putten H., Schwab M.E.;
RT      "Genomic Structure and Functional Characterization of the Promoter
RT      Structures of Human and Mouse Nogo/Rtn-4.";
RL      Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN=129/SvcJ7, and 129SvcJ7;
RA      Oertle T., Schwab M.E.;
RL      Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN      [3]
RP      SEQUENCE FROM N.A.
RC      STRAIN=129/SvcJ7;
RA      Van der Putten H.;
RL      Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN      [4]
RP      SEQUENCE FROM N.A.
RC      STRAIN=129SvcJ7;
RA      Van der Putten H., Mir A.;
RL      Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR      EMBL; AY102281; AAM73503.1; -.

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DR EMBL; AY102286; AAM73508.1; -.
SQ SEQUENCE 356 AA; 38403 MW; 4366C03BA9630B56 CRC64;

Query Match 62.8%; Score 443; DB 11; Length 356;
Best Local Similarity 98.9%; Pred. No. 6.6e-37;
Matches 92; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy      49 VVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 108
          |||
Db      169 VVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 228

Qy      109 AKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141
          |||
Db      229 QKSDEGHPFRAYLESEVAISEELVQKYSNSALG 261
```

RESULT 6

Q8BHF5

ID Q8BHF5 PRELIMINARY; PRT; 375 AA.
AC Q8BHF5;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE RTN4.
GN RTN4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvcJ7, and 129SvcJ7;
RA Oertle T., van der Putten H., Schwab M.E.;
RT "Genomic Structure and Functional Characterization of the Promoter
RT Structures of Human and Mouse Nogo/Rtn-4.";
RL Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvcJ7, and 129SvcJ7;
RA Oertle T., Schwab M.E.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvcJ7;
RA Van der Putten H.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=129SvcJ7;
RA Van der Putten H., Mir A.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY102282; AAM73504.1; -.
DR EMBL; AY102286; AAM73509.1; -.
SQ SEQUENCE 375 AA; 40300 MW; 23D9EB19BE671AE6 CRC64;

Query Match 62.8%; Score 443; DB 11; Length 375;
Best Local Similarity 98.9%; Pred. No. 7e-37;

Matches 92; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      49 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAI 108
          |||
Db      188 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAI 247

Qy      109 AKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141
          |||
Db      248 QKSDEGHPFRAYLESEVAISEELVQKYSNSALG 280
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RESULT 7

Q96B16

ID Q96B16 PRELIMINARY; PRT; 392 AA.
AC Q96B16;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein (RTN4).
GN RTN4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia ~~Primate~~ Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Oertle T., van der Putten H., Schwab M.E.;
RT "Genomic Structure and Functional Characterization of the Promoter
RT Structures of Human and Mouse Nogo/Rtn-4.";
RL Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Oertle T., Schwab M.E.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Van der Putten H.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=22376540; PubMed=12488097;
RA Oertle T., van der Putten H., Schwab M.E.;
RT "Genomic Structure and Functional Characterization of the Promoter
RT Structures of Human and Mouse Nogo/Rtn-4.";
RL J. Mol. Biol. 325:299-323(2003).
DR EMBL; BC016165; AAH16165.1; -.
DR EMBL; AY102285; AAM64242.1; -.
DR EMBL; AY102278; AAM64247.1; -.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
KW Hypothetical protein.

AC Q8K3G7;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Nogo-B.
 GN RTN4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RA Jin W., Li R., Long M., Shen J., Ju G.;
 RT "Cloning and expression of the mouse Nogo-B protein."
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AY114153; AAM77069.1; -.
 DR MGD; MGI:1915835; Rtn4.
 DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS50845; RETICULON; 1.
 SQ SEQUENCE 357 AA; 38566 MW; 73BB3D17DFDBDF15 CRC64;

Query Match p2125X561.3%; Score 432.5; DB 11; Length 357; G ;875X
 Best Local Similarity 97.9%; Pred. No. 7.8e-36;
 Matches 92; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 49 VVDLLYWRDIKKTGVV-FGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIA 107
 ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
 Db 169 VVDLLYWRDIKKTGVVYFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIA 228

 Qy 108 IAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141
 | ||||||||||||||||||||||||||||||||
 Db 229 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALG 262

RESULT 10

Q9GM33
 ID Q9GM33 PRELIMINARY; PRT; 179 AA.
 AC Q9GM33;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical 19.9 kDa protein.
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
 OC Cercopithecinae; Macaca.
 OX NCBI_TaxID=9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
 RA Suzuki Y., Sugano S., Hashimoto K.;
 RT "Isolation of full-length cDNA clones from macaque brain cDNA
 RT libraries."
 RL Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AB049853; BAB16739.1; -.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
KW Hypothetical protein.
SQ SEQUENCE 179 AA; 19949 MW; 5F8CD4383FEE9E02 CRC64;

Query Match 54.8%; Score 386; DB 6; Length 179;
Best Local Similarity 96.4%; Pred. No. 2e-31;
Matches 81; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 58 IKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIAKSDEGHPF 117
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Db 1 MKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYRGVIAIQKSDEGHPF 60

Qy 118 RAYLESEVAISEELVQKYSNSALG 141
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Db 61 RAYLESEVAISEELVQKYSNSALG 84

RESULT 11

Q9BQ59

ID Q9BQ59 PRELIMINARY; PRT; 199 AA.

AC Q9BQ59;

DT2 -JUN-2001/(MrEMBLrel. 17, Created)

DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Similar to reticulon 1.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Lung;

RA Strausberg R.;

RL Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.

DR EMBL; BC003003; AAH03003.1; -.

DR EMBL; BC000314; AAH00314.1; -.

DR InterPro; IPR001951; Histone_H4.

DR InterPro; IPR003388; Reticulon.

DR Pfam; PF02453; Reticulon; 1.

DR PROSITE; PS00047; HISTONE_H4; 1.

DR PROSITE; PS50845; RETICULON; 1.

SQ SEQUENCE 199 AA; 22642 MW; 7CFA44CC568DF6D8 CRC64;

Query Match 49.4%; Score 348; DB 4; Length 199;
Best Local Similarity 64.0%; Pred. No. 1.7e-27;
Matches 64; Conservative 18; Mismatches 18; Indels 0; Gaps 0;

Qy 38 MDGQKKHWKDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS 97
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Db 1 MDCVWSNWSQAIDLLYWRDIKQTGIVFGSFLLLLFSLTQFSVSVVAYLALAALSATIS 60

Qy 98 FRIYKGVIAIAKSDEGHPFRAYLESEVAISEELVQKYSN 137
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Db 61 FRIYKSVLQAVQKTDEGHPFKAYLELEITLSQEQIQKYTD 100

RESULT 12

Q63765

ID Q63765 PRELIMINARY; PRT; 267 AA.
AC Q63765;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Rat C1-13 gene product.
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CD; TISSUE=Brain;
RX MEDLINE=91278684; PubMed=1647480;
RA Wieczorek D.F., Hughes S.R.;
RT "Developmentally regulated cDNA expressed exclusively in neural
RT tissue.";
RL Brain Res. Mol. Brain Res. 10:33-41(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CD; TISSUE=Brain;
RA Wieczorek D.F.;
RL Submitted (FEB-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; X52817; CAA37001.1; -.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
SQ SEQUENCE 267 AA; 30328 MW; A591C6E37DB7A175 CRC64;

Query Match 49.4%; Score 348; DB 11; Length 267;
Best Local Similarity 64.0%; Pred. No. 2.3e-27;
Matches 64; Conservative 18; Mismatches 18; Indels 0; Gaps 0;

Qy 38 MDGQKKHWKDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS 97
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Db 1 MDCVWSNWKQSAIDLLYWRDIKQTGIVFGSFLLLSLTQFSVSVVAYLALAALSATIS 60
Qy 98 FRIYKGVIAIAKSDEGHPFRAYLESEVAISEELVQKYSN 137
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Db 61 FRIYKSVLQAVQKTDEGHPFKAYLELEITLSQEIQKYTD 100

RESULT 13

Q8K4S4

ID Q8K4S4 PRELIMINARY; PRT; 780 AA.
AC Q8K4S4;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Reticulon 1A.
GN RTN1 OR RTN-1A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ICR; TISSUE=Brain;
 RA Hirata T., Nomura T., Takagi Y., Sato Y., Tomioka N., Fujisawa H.,
 RA Osumi N.;
 RT "Mosaic development of the olfactory cortex with Pax6-dependent and
 RT -independent components.";
 RL Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AB074899; BAB96551.1; -.
 DR MGD; MGI:1933947; Rtn1.
 DR InterPro; IPR001951; Histone_H4.
 DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS00047; HISTONE_H4; 1.
 DR PROSITE; PS50845; RETICULON; 1.
 SQ SEQUENCE 780 AA; 83504 MW; 545F5638C576A069 CRC64;

Query Match 47.8%; Score 337; DB 11; Length 780;
 Best Local Similarity 67.4%; Pred. No. 1e-25;
 Matches 62; Conservative 16; iXMismatches 14; Indels 0; Gaps 0;

Qy 46 KDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKQVI 105
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 Db 590 KQKAIDLLYWRDIKQTGIVFGSFLLLSLTQFSVSVVAYLALAALSATISFRIYKSVL 649
 Qy 106 QAIAKSDEGHPFRAYLESEVAISEELVQKYSN 137
 || : | : ||||| : ||| | : : | : ||| : :
 Db 650 QAVQKTDEGHPFKAYLELEITLSQEIQKYTD 681

RESULT 14

Q8K0T0

ID Q8K0T0 PRELIMINARY; PRT; 780 AA.
 AC Q8K0T0;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Similar to reticulon 1.
 GN RTN1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10 TI
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Retina;
 RA Strausberg R.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC030455; AAH30455.1; -.
 DR MGD; MGI:1933947; Rtn1.
 DR InterPro; IPR001951; Histone_H4.
 DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS00047; HISTONE_H4; 1.
 DR PROSITE; PS50845; RETICULON; 1.

Query Match 47.8%; Score 337; DB 11; Length 780;
Best Local Similarity 67.4%; Pred. No. 1e-25;
Matches 62; Conservative 16; Mismatches 14; Indels 0; Gaps 0;

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QY      46 KDKVVDLLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKQVI 105
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Db     590 KQKAIDL LLYWRDIKQTGIVFGSFL LLLFSLTQFSVVS VVAYLALAALSATISFRIYKSVL 649
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QY     106 QAIAKSDEGHPFRAYLESEVAISEELVQKYSN 137
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Db     650 QAVOKTDEGHPFKAYLELEITLSQEIQKYTD 681

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090637

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ID      Q90637; PRELIMINARY; PRT; 208 AA.
AC      Q90637;
DT      01-NOV-1996 (TrEMBLrel. 01, Created)
DT      01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT      01-MAR-2003 (TrEMBLrel. 23, La t annotation update)
DE      ChS-Rex-s.
OS      Gallus gallus (Chicken).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC      Gallus.
OX      NCBI_TaxID=9031;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Brain;
RX      MEDLINE=96386034; PubMed=8793864;
RA      Baka I.D., Ninkina N.N., Pinon L.G., Adu J., Davies A.M.,
RA      Georgiev G.P., Buchman V.L.;
RT      "Intracellular compartmentalization of two differentially spliced s-
RT      rex/NSP mRNAs in neurons.";
RL      Mol. Cell. Neurosci. 7:289-303(1996).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Brain;
RX      MEDLINE=97183663;
RA      Ninkina N.N., Baka I.D., Buchman V.L.;
RT      "Rat and chicken s-rex/NSP mRNA: nucleotide sequence of main
RT      transcripts and expression of splice variants in rat tissues.";
RL      Gene 184:205-210(1997).
DR      EMBL; U17605; AAC60074.1; -.
DR      InterPro; IPR003388; Reticulon.
DR      Pfam; PF02453; Reticulon; 1.
DR      PROSITE; PS50845; RETICULON; 1.
SQ      SEQUENCE 208 AA; 23593 MW; 9C90FDAEE15DAB45 CRC64;

Query Match 46.1%; Score 325; DB 13; Length 208;
Best Local Similarity 59.4%; Pred. No. 3.8e-25;
Matches 60; Conservative 23; Mismatches 18; Indels 0; Gaps 0;

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QY 37 EMDGQKKHWDKDVDDLLVWRDI KKTGVVFSGASLFLSLTLVSIVSVTAYIALALLSVTI 96
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 : | | : | | : : | | | : | : | : | : | : | : | : | : | : | : | : | : | :

Db 9 KMDCLWSNWKCQAINLLYWREIKQTGIVFGSLLLLLFSLTQFSVSVVAYLALAGLSATI 68

Qy 97 SFRIYKGVIAIAKSDEGHPFRAYLESEVAISEELVQKYSN 137

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Db 69 SFRIYKSVLQAVQKTDEGHPFKAYLDMEMNLSQDQIQKYTD 109

Search completed: January 22, 2004, 16:34:13

Job time : 8.37604 secs

OM protein - protein search, using sw model

Run on: January 22, 2004, 16:34:19 ; Search time 6.94845 Seconds
(without alignments)
4195.163 Million cell updates/sec

Title: US-09-830-972-32
Perfect score: 705
Sequence: 1 QASGEAGVSLRENFAVYSV.....ESEVAISEELVQKYSNSALG 141

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 777136 seqs, 206736638 residues

Total number of hits satisfying chosen parameters: 777136

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
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- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query					
No.	Score	Match	Length	DB	ID		Description

1	510	72.3	199	9	US-09-893-348-21	Sequence 21, Appl
2	503	71.3	118	12	US-10-264-237-1568	Sequence 1568, Ap
3	503	71.3	199	9	US-09-893-348-25	Sequence 25, Appl
4	447	63.4	1163	9	US-09-893-348-18	Sequence 18, Appl
5	447	63.4	1192	9	US-09-789-386-2	Sequence 2, Appli
6	447	63.4	1192	9	US-09-758-140-6	Sequence 6, Appli
7	447	63.4	1192	9	US-09-893-348-23	Sequence 23, Appl
8	447	63.4	1192	9	US-09-972-599A-6	Sequence 6, Appli
9	447	63.4	1192	15	US-10-060-036-71	Sequence 71, Appl
10	443	62.8	360	9	US-09-893-348-20	Sequence 20, Appl
11	443	62.8	373	9	US-09-789-386-6	Sequence 6, Appli
12	443	62.8	373	9	US-09-765-205-6	Sequence 6, Appli
13	443	62.8	373	9	US-09-893-348-24	Sequence 24, Appl
14	443	62.8	373	15	US-10-060-036-72	Sequence 72, Appl
15	443	62.8	379	12	US-10-205-194-164	Sequence 164, App
16	348	49.4	267	12	US-10-205-194-127	Sequence 127, App
17	337	47.8	777	12	US-10-205-219-93	Sequence 93, Appl
18	309	43.8	236	9	US-09-729-674-20	Sequence 20, Appl
19	309	43.8	236	9	US-09-765-205-26	Sequence 26, Appl
20	309	43.8	269	15	US-10-106-698-6222	Sequence 6222, Ap
21	304	43.1	593	12	US-10-108-260A-2892	Sequence 2892, Ap
22	269	38.2	161	9	US-09-925-302-808	Sequence 808, App
23	227	32.2	168	11	US-09-809-391-563	Sequence 563, App
24	227	32.2	168	12	US-09-882-171-563	Sequence 563, App
25	213	30.2	66	9	US-09-758-140-20	Sequence 20, Appl
26	213	30.2	66	9	US-09-972-599A-20	Sequence 20, Appl
27	207	29.4	66	9	US-09-972-599A-22	Sequence 22, Appl
28	207	29.4	66	11	US-09-972-546-7	Sequence 7, Appli
29	193	27.4	40	9	US-09-758-140-8	Sequence 8, Appli
30	193	27.4	40	9	US-09-758-140-18	Sequence 18, Appl
31	193	27.4	40	9	US-09-972-599A-18	Sequence 18, Appl
32	177	25.1	72	12	US-10-029-386-28762	Sequence 28762, A
33	156.5	22.2	36	9	US-09-972-599A-28	Sequence 28, Appl
34	155.5	22.1	36	9	US-09-972-599A-30	Sequence 30, Appl
35	135.5	19.2	31	9	US-09-972-599A-32	Sequence 32, Appl
36	133.5	18.9	31	9	US-09-972-599A-26	Sequence 26, Appl
37	125	17.7	25	9	US-09-972-599A-8	Sequence 8, Appli
38	123	17.4	25	9	US-09-972-599A-24	Sequence 24, Appl
39	118	16.7	25	9	US-09-758-140-10	Sequence 10, Appl
40	118	16.7	25	9	US-09-972-599A-10	Sequence 10, Appl
41	115.5	16.4	26	9	US-09-972-599A-34	Sequence 34, Appl
42	113	16.0	25	9	US-09-758-140-12	Sequence 12, Appl
43	113	16.0	25	9	US-09-972-599A-12	Sequence 12, Appl
44	81.5	11.6	464	12	US-10-369-493-5428	Sequence 5428, Ap
45	72.5	10.3	714	12	US-10-369-493-3467	Sequence 3467, Ap

ALIGNMENTS

RESULT 1
 US-09-893-348-21
 ; Sequence 21, Application US/09893348
 ; Patent No. US20020072493A1
 ; GENERAL INFORMATION:
 ; APPLICANT: EISENBACH-SCHWARTZ, Michal

```
; APPLICANT: COHEN, Irun R.
; APPLICANT: BESERMAN, Pierre
; APPLICANT: MOSONEGO, Alon
; APPLICANT: MOALEM, Gila
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND
THEIR USES
; FILE REFERENCE: EIS-SCHWARTZ=2A
; CURRENT APPLICATION NUMBER: US/09/893,348
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/314,161
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 09/218,277
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: PCT/US98/14715
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: IL 124500
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-893-348-21
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Query Match          72.3%; Score 510; DB 9; Length 199;
Best Local Similarity 99.0%; Pred. No. 3.7e-51;
Matches 103; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy      38 MDGQKKHKWCDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS 97
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Db      1 MDGQKKHKWCDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS 60

Qy      98 FRIYKGVIAIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141
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Db      61 FRIYKGVIAIAKSDGHPFRAYLESEVAISEELVQKYSNSALG 104
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RESULT 2

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US-10-264-237-1568
; Sequence 1568, Application US/10264237
; Publication No. US20040009491A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA131P1
; CURRENT APPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 1568
; LENGTH: 118
; TYPE: PRT
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Db      61 FRIYKGVIAIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 104

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RESULT 4

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US-09-893-348-18
; Sequence 18, Application US/09893348
; Patent No. US20020072493A1
; GENERAL INFORMATION:
; APPLICANT: EISENBACH-SCHWARTZ, Michal
; APPLICANT: COHEN, Irun R.
; APPLICANT: BESERMAN, Pierre
; APPLICANT: MOSONEGO, Alon
; APPLICANT: MOALEM, Gila
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND
THEIR USES
; FILE REFERENCE: EIS-SCHWARTZ=2A
; CURRENT APPLICATION NUMBER: US/09/893,348
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/314,161
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 09/218,277
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: PCT/US98/14715
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: IL 124500
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 1163
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-893-348-18

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Query Match          63.4%; Score 447; DB 9; Length 1163;
Best Local Similarity 96.9%; Pred. No. 8.3e-43;
Matches 93; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy      46 KDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV 105
          | |||||
Db      973 KTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV 1032

Qy      106 QAIKSDGEGH1475Xv EVAISEELVQKYSNSALG 141
          ||| |||||
Db      1033 QAIQKSDGEGHPFRAYLESEVAISEELVQKYSNSALG 1068

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RESULT 5

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US-09-789-386-2
; Sequence 2, Application US/09789386
; Patent No. US20020010324A1
; GENERAL INFORMATION:

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Query Match 63.4%; Score 447; DB 9; Length 1192;
Best Local Similarity 96.9%; Pred. No. 8.6e-43;
Matches 93; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy      46 KDKVVDLLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI 105
         | |||||
Db     1002 KTSVVDLLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI 1061
         |||
Qy      106 QAIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141
         |||
Db     1062 QAIOKSDEGHPFRAYLESEVAISEELVQKYSNSALG 1097
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RESULT 7

US-09-893-348-23

; Sequence 23, Application US/09893348

; Patent No. US20020072493A1

; GENERAL INFORMATION:

APPLICANT: EISENBACH-SCHWARTZ, Michal

APPLICANT: COHEN, Irun R.

; APPLICANT: BESERMAN, Pierre

APPLICANT: MOSONEGO, Alon

; APPLICANT: MOALEM, Gila

; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND
 THEIR USES

FILE REFERENCE: EIS-SCHWARTZ=2A

; CURRENT APPLICATION NUMBER: US/09/893,348

; CURRENT FILING DATE: 2001-06-28

; PRIOR APPLICATION NUMBER: US 09/314,161

; PRIOR FILING DATE: 1999-05-19

; PRIOR APPLICATION NUMBER: US 09/218,277

; PRIOR FILING DATE: 1998-12-22

; PRIOR APPLICATION NUMBER: PCT/US98/14715

; PRIOR FILING DATE: 1998-07-21

; PRIOR APPLICATION NUMBER: IL 124500

; PRIOR FILING DATE: 1998-05-19

; NUMBER OF SEQ ID NOS: 29

```
; SOFTWARE: PatentIn version 3.1
```

; SEQ ID NO 23

; LENGTH: 1192

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; TYPE: PRT

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; ORGANISM: Homo sapiens

US-09-893-348-23

Query Match 63.4%; Score 447; DB 9; Length 1192;
Best Local Similarity 96.9%; Pred. No. 8.6e-43;
Matches 93; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

[illegible]

RESULT 8

US-09-972-599A-6

; Sequence 6, Application US/09972599A
 ; Patent No. US20020077295A1
 ; GENERAL INFORMATION:
 ; APPLICANT: STRITTMATTER, STEPHEN M.
 ; TITLE OF INVENTION: NOGO-RECEPTOR-MEDIATED BLOCKADE OF AXONAL GROWTH
 ; FILE REFERENCE: C077 CIP US
 ; CURRENT APPLICATION NUMBER: US/09/972,599A
 ; CURRENT FILING DATE: 2001-10-06
 ; PRIOR APPLICATION NUMBER: PCT/US01/01041
 ; PRIOR FILING DATE: 2001-01-12
 ; PRIOR APPLICATION NUMBER: 09/758,140
 ; PRIOR FILING DATE: 2001-01-12
 ; PRIOR APPLICATION NUMBER: 60/236,378
 ; PRIOR FILING DATE: 2000-09-29
 ; PRIOR APPLICATION NUMBER: 60/207,366
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: 60/175,707
 ; PRIOR FILING DATE: 2000-01-12
 ; NUMBER OF SEQ ID NOS: 57
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 6
 ; LENGTH: 1192
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-972-599A-6

Query Match 63.4%; Score 447; DB 9; Length 1192;
 Best Local Similarity 96.9%; Pred. No. 8.6e-43;
 Matches 93; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 46 KDKVVDLLYWDRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV 105
 | |||||
 Db 1002 KTSVVDLLYWDRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV 1061
 Qy 106 QAIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141
 ||| |||||
 Db 1062 QAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALG 1097

RESULT 9

US-10-060-036-71

; Sequence 71, Application US/10060036
 ; Publication No. US20030073144A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Benson, Darin R.
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Lodes, Michael J.
 ; APPLICANT: Persing, David H.
 ; APPLICANT: Hepler, William T.
 ; APPLICANT: Jiang, Yuqiu
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
 ; FILE REFERENCE: 210121.566
 ; CURRENT APPLICATION NUMBER: US/10/060,036


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Qy      49 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAI 108
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      173 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAI 232

Qy      109 AKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141
          ||||||||||||||||||||||||||||||||||||
Db      233 QKSDEGHPFRAYLESEVAISEELVQKYSNSALG 265

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RESULT 11

US-09-789-386-6

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; Sequence 6, Application US/09789386
; Patent No. US20020010324A1
; GENERAL INFORMATION:
; APPLICANT: MICHALOVICH, DAVID
; APPLICANT: PRINJHA, RABINDER KUMAR
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30165-C1
; CURRENT APPLICATION NUMBER: US/09/789,386
; CURRENT FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: U.K. 9916898.1
; PRIOR FILING DATE: 1999-07-19
; PRIOR APPLICATION NUMBER: U.K. 9816024.5
; PRIOR FILING DATE: 1998-07-22
; PRIOR APPLICATION NUMBER: US 09/359,208
; PRIOR FILING DATE: 1999-07-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 373
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-789-386-6

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```

Query Match          62.8%; Score 443; DB 9; Length 373;
Best Local Similarity 98.9%; Pred. No. 5.4e-43;
Matches 92; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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```

Qy      49 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAI 108
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      186 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAI 245

Qy      109 AKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141
          ||||||||||||||||||||||||||||||||||||
Db      246 QKSDEGHPFRAYLESEVAISEELVQKYSNSALG 278

```

RESULT 12

US-09-765-205-6

```

; Sequence 6, Application US/09765205
; Patent No. US20020034800A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Li
; TITLE OF INVENTION: BONE MARROW SECRETED PROTEINS AND POLYNUCLEOTIDES
; FILE REFERENCE: 1458.004/200130.449
; CURRENT APPLICATION NUMBER: US/09/765,205
; CURRENT FILING DATE: 2001-01-17

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; PRIOR APPLICATION NUMBER: US/09/212,440
; PRIOR FILING DATE: 1998-12-16
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 373
; TYPE: PRT
; ORGANISM: human
US-09-765-205-6

Query Match 62.8%; Score 443; DB 9; Length 373;
Best Local Similarity 98.9%; Pred. No. 5.4e-43;
Matches 92; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 49 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAI 108
|||||
Db 186 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAI 245

Qy 109 AKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141
|||||
Db 246 QKSDEGHPFRAYLESEVAISEELVQKYSNSALG 278

RESULT 13

US-09-893-348-24

; Sequence 24, Application US/09893348
; Patent No. US20020072493A1
; GENERAL INFORMATION:
; APPLICANT: EISENBACH-SCHWARTZ, Michal
; APPLICANT: COHEN, Irun R.
; APPLICANT: BESERMAN, Pierre
; APPLICANT: MOSONEGO, Alon
; APPLICANT: MOALEM, Gila
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND
THEIR USES
; FILE REFERENCE: EIS-SCHWARTZ=2A
; CURRENT APPLICATION NUMBER: US/09/893,348
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/314,161
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 09/218,277
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: PCT/US98/14715
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: IL 124500
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 373
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-893-348-24

Query Match 62.8%; Score 443; DB 9; Length 373;
Best Local Similarity 98.9%; Pred. No. 5.4e-43;
Matches 92; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 49 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAI 108
 |||
 Db 186 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAI 245

Qy 109 AKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141
 |||
 Db 246 QKSDEGHPFRAYLESEVAISEELVQKYSNSALG 278

RESULT 14

US-10-060-036-72

; Sequence 72, Application US/10060036
 ; Publication No. US20030073144A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Benson, Darin R.
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Lodes, Michael J.
 ; APPLICANT: Persing, David H.
 ; APPLICANT: Hepler, William T.
 ; APPLICANT: Jiang, Yuqiu
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
 ; FILE REFERENCE: 210121.566
 ; CURRENT APPLICATION NUMBER: US/10/060,036
 ; CURRENT FILING DATE: 2002-01-30
 ; NUMBER OF SEQ ID NOS: 4560
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 72
 ; LENGTH: 373
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

US-10-060-036-72

Query Match 62.8%; Score 443; DB 15; Length 373;
 Best Local Similarity 98.9%; Pred. No. 5.4e-43;
 Matches 92; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 49 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAI 108
 |||
 Db 186 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAI 245

Qy 109 AKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141
 |||
 Db 246 QKSDEGHPFRAYLESEVAISEELVQKYSNSALG 278

RESULT 15

US-10-205-194-164

; Sequence 164, Application US/10205194
 ; Publication No. US20030134301A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Warner-Lambert Company
 ; APPLICANT: Lee, Kevin
 ; APPLICANT: Dixon, Alistair
 ; APPLICANT: Brooksbank, Robert
 ; APPLICANT: Pinnock, Robert

```

; TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
; FILE REFERENCE: WL-A-018201
; CURRENT APPLICATION NUMBER: US/10/205,194
; CURRENT FILING DATE: 5200-07-24
; PRIOR APPLICATION NUMBER: GB 0118354.0
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 164
; LENGTH: 379
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Foocen-m2 reticulon
US-10-205-194-164

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Query Match          62.8%; Score 443; DB 12; Length 379;
Best Local Similarity 98.9%; Pred. No. 5.5e-43;
Matches 92; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      49 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 108
          |||
Db      192 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 251
          |||

Qy      109 AKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141
          |||
Db      252 QKSDEGHPFRAYLESEVAISEELVQKYSNSALG 284
          |||

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Search completed: January 22, 2004, 16:44:58
Job time : 7.94845 secs

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OM protein - protein search, using sw model

Run on: January 22, 2004, 16:31:15 ; Search time 2.35178 Seconds
 (without alignments)
 2819.465 Million cell updates/sec

Title: US-09-830-972-32
 Perfect score: 705
 Sequence: 1 QASGEAGVSLRENFAVYSV.....ESEVAISEELVQKYSNSAIG 141

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	495	70.2	199	1	RTN4_MOUSE	Q99p72	mus musculus
2	447	63.4	1163	1	RTN4_RAT	Q9jkl1	rattus norv
3	447	63.4	1192	1	RTN4_HUMAN	Q9nqc3	homo sapien
4	337	47.8	776	1	RTN1_HUMAN	Q16799	homo sapien
5	337	47.8	777	1	RTN1_RAT	Q64548	rattus norv
6	309	43.8	236	1	RTN3_HUMAN	O95197	homo sapien
7	308	43.7	237	1	RTN3_MOUSE	Q9es97	mus musculus
8	214	30.4	545	1	RTN2_HUMAN	O75298	homo sapien
9	197	27.9	471	1	RTN2_MOUSE	O70622	mus musculus
10	77.5	11.0	243	1	T2RD_MOUSE	Q9jka2	mus musculus
11	77.5	11.0	261	1	PHSC_ECOLI	P77409	escherichia
12	75.5	10.7	246	1	T2R8_MOUSE	Q9jka0	mus musculus
13	75.5	10.7	545	1	G6PI_HELPY	O25781	helicobacte
14	74.5	10.6	545	1	G6PI_HELPJ	Q9zk49	helicobacte
15	74	10.5	268	1	YC73_HAEIN	P44150	haemophilus
16	72	10.2	614	1	S6AC_RABIT	P48055	oryctolagus
17	72	10.2	3511	1	MY15_MOUSE	Q9qzz4	mus musculus

18	71	10.1	346	1	3BHS_VACCC	P21097	v 3 beta-hy
19	71	10.1	346	1	3BHS_VACCV	P26670	v 3 beta-hy
20	70	9.9	960	1	GBR1_MOUSE	Q9wv18	mus musculu
21	70	9.9	961	1	GBR1_HUMAN	Q9ubs5	homo sapien
22	70	9.9	991	1	GBR1_RAT	Q9z0u4	rattus norv
23	69	9.8	315	1	LXD1_PHOLE	P21309	photobacter
24	69	9.8	398	1	PGK_STRPN	Q97s89	streptococc
25	69	9.8	468	1	YDBM_CAEEL	Q19084	caenorhabdi
26	68.5	9.7	238	1	T2RA_MOUSE	Q9jka3	mus musculu
27	68.5	9.7	311	1	HTRB_HAEIN	P45239	haemophilus
28	68.5	9.7	325	1	VP35_VARV	P33059	variola vir
29	68	9.6	184	1	YDB5_SCHPO	Q10358	schizosacch
30	68	9.6	1447	1	DCC_HUMAN	P43146	homo sapien
31	67.5	9.6	324	1	VP35_VACCC	P20497	vaccinia vi
32	67.5	9.6	503	1	LEU1_BUCUM	Q9evh0	buchnera ap
33	67.5	9.6	877	1	SULH_SCHPO	O74377	schizosacch
34	67	9.5	175	1	OLE2_BRANA	P29111	brassica na
35	67	9.5	453	1	SYS_ARCFU	O28244	archaeoglob
36	67	9.5	525	1	SYH_CAEEL	P34183	caenorhabdi
37	67	9.5	756	1	RIR1_HAEIN	P43754	haemophilus
38	66.5	9.4	3174	1	CHAC_HUMAN	Q96rl7	homo sapien
39	66	9.4	253	1	ADH_DROAD	Q00669	drosophila
40	66	9.4	537	1	YCUB_SCHPO	O59831	schizosacch
41	66	9.4	548	1	AMDS_EMENI	P08158	emericeella
42	65.5	9.3	182	1	Y696_METJA	Q58107	methanococc
43	65.5	9.3	664	1	NTPI_ENTHR	P43439	enterococcu
44	65.5	9.3	880	1	DPO1_BACSU	O34996	bacillus su
45	65.5	9.3	1037	1	YOJ8_YEAST	Q12496	saccharomyc

ALIGNMENTS

RESULT 1

RTN4_MOUSE

ID RTN4_MOUSE STANDARD; PRT; 199 AA.
AC Q99P72; Q9CTE3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein).
GN RTN4 OR NOGO.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3T3-L1; TISSUE=Adipocyte;
RA Coulson A.C., Craggs P.D., Morris N.J.;
RT "Mouse vp20/RTN4C cDNA.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE OF 170-199 FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,